

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean-Baptiste
Duclert, Aymeric
Bougueleret, Lydie

<120> EXTENDED CDNAS FOR SECRETED PROTEINS

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<140> 09/191,997

<141> 1998-11-13

<150> 60/066,677

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<150> 60/069,957

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<150> 60/074,121

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<150> 60/081,563

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 tttttvn 67

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gagagaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc    113
                               Met Lys Lys Val Leu Leu Leu Ile
                               -15                               -10

aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag    161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                               -5                               1                               5

gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr    209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
                               10                               15                               20

wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca coa att    257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
                               25                               30                               35

cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata    305

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ctgatgccga	gttccgtctc	tcgcgtcttt	tcctgggtccc	aggcaaagcg	gasgnagatc	120
ctcaaacggc	ctagtgtctc	ggcgttccgg	agaaaatcag	cggtctaatt	aattcctctg	180
gtttgttgaa	gcagttacca	agaatcttca	accctttccc	acaaaagcta	attgagtaca	240
cgttcctggt	gagtacacgt	tcctgttgat	ttacaaaagg	tgcagggtatg	agcagggtctg	300
aagactaaca	ttttgtgaag	ttgtaaaaca	gaaaacctgt	tagaa atg tgg tgg ttt		357
				Met Trp Trp Phe		
				-20		

cag	caa	ggc	ctc	agt	ttc	ctt	cct	tca	gcc	ctt	gta	att	tgg	aca	tct	405
Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val	Ile	Trp	Thr	Ser	
	-15						-10				-5					

gct	gct	ttc	ata	ttt	tca	tac	att	act	gca	gta	aca	ctc	cac	cat	ata	453
Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His	Ile	
1			5						10						15	

gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggt	aca	gta	gct	cca	raa	501
Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro	Xaa	
			20					25				30				

aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	ggt	tta	tgt	caa	549
Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys	Gln	
		35					40					45				

aaa	tagaaatcag	gaarataatt	caacttaaag	aakttcattt	catgaccaa	602
Lys						

ctcttcaraa	acatgtcttt	acaagcatat	ctcttgattt	gcttttctaca	ctgttgaatt	662
gtctggcaat	atttctgcag	tggaaaattt	gatttarmta	gttcttgact	gataaatatg	722
gtaaggtggg	cttttcccc	tgtgtaattg	gctactatgt	cttactgagc	caagttgtaw	782
tttgaaataa	aatgatatga	gagtgacaca	aaaaaaaaaa			822

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score 5.5
seq SFLPSALVIWTSA/AF
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Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val

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1 5
Ile Trp Thr Ser Ala
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10

15

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cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct 120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
-35 -30 -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
-20 -15 -10
ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg 325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
-5 1 5 10
cct gac aac taaatatact tatccaaatc aataaarwra raatcctccc 374
Pro Asp Asn
tcgaraaggg tttctaaaaa caaaaaaaaaa a 405

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<222> 1..37
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score 5.9
seq LSYASSALSPCLT/AP
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Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1 5 10 15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
20 25 30
Ser Pro Cys Leu Thr
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attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg 120
cccgagagata ggaccaaccg tcaggaatgc gaggaatggt tttcttcgga ctctatcgag 180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt 231
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
-15 -10 -5
gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt 279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
1 5 10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg 327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
15 20 25
gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat 375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
30 35 40 45
tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc 424
Ser Ser Ala
atatttaa at tggaagagtc aaattgasca ttattaaata aagcttggtt aatatgtctc 484
aaacaaaaaa aa 496

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score 5.5
seq ILSTVTALTFFAXA/LD
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Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
1 5 10 15

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005760-00999960

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Met Leu Trp Leu Leu Phe Phe
-10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat 100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
-5 1 5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca 148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
10 15 20 25
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct 196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
30 35 40
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat 244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
45 50 55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt 292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
60 65 70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca 340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
75 80 85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat 388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
90 95 100 105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc 436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
110 115 120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt 484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
125 130 135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg 532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
140 145 150
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa 580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
155 160 165
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat 628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
170 175 180 185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag 676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
190 195 200
gat gag agg ctc acc cct ctc tgaagggctg ttgttctgct tcttcaaraa 727
Asp Glu Arg Leu Thr Pro Leu
205
attaaacatt tgttttctgtg tgactgctga gcatcctgaa ataccaagag cagatcatat 787
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c 848
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score 0.983
sequence tgtcagttg

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name MYOD_Q6
score 0.961
sequence cccaactgac

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<222> complement(75..85)

005760-0099960

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score 0.960
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<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag
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score 0.960
sequence gcacacctcag
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name GATA_C
score 0.964
sequence agataaatcca
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score 0.958
sequence cttcagttg
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name GATA1_02
score 0.959
sequence ttgtagataggaca
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name GATA_C
score 0.953
sequence agataggacat
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score 0.973
sequence cataacagatggtaag
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name TAL1BETAE47_01

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score 0.983
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score 0.954
sequence accatctgtt
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name GATA1_04
score 0.953
sequence tcaagataaagta
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score 0.963
sequence agttgggaattcc
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name IK2_01
score 0.985
sequence agttgggaattc
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score 0.962
sequence tgggaattcc
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sequence tcagtgatatggca
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<222> complement(478..489)
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name SRY_02
score 0.951
sequence taaaacaaaaca

005150 0099950

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name E2F_02
score 0.957
sequence tttagcgc

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sequence tgagggga

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tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat gggtctatta 120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
atcaggagaa aaaaatgaca tctggaaaac ctatagggga aggcataaca gatggtaagg 300
atactttatc ttgagtagga gagccttctc gtggcaacgt ggagaaggga agaggtcgta 360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
catcagtgat atggcaaagt tgggaactaag ggtagtgatc agaggggttaa aattgtgtgt 480
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cttcat 546

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gtaccaggga ctgtgaccat tgc 23

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ctgtgaccat tgctcccaag agag 24

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<223> matinspector prediction

005150-091500 005150-091500

name NFX_Q6
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score 0.962
sequence cctgggga
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score 0.994
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score 0.985
sequence tccaacggt
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score 0.968
sequence ttcctggaa
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name STAT_01
score 0.951
sequence ttccaggaa
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name MZF1_01
score 0.956
sequence ttggggga
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name IK2_01
score 0.965
sequence gaatgggatttc
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name MZF1_01
score 0.986

005150-0099990

sequence agagggga
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name SRY_02
score 0.955
sequence gaaaacaaaaca
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score 0.960
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score 0.981
sequence agcatctgcc
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name S8_01
score 0.992
sequence gaggcaattat
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<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga
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<400> 34
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tgattgggtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct 120
cggtgaccgt tggattcctg gaagcagtag ctgttctggt tggatctggt agggacaggg 180
ctcagagggc taggcacgag ggaaggctcag aggagaaggs aggsarggcc cagtgagarg 240
ggagcatgcc ttcccccaac cctggcttsc ycttggyam agggcgkttt tgggmacttr 300
aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacia tagcctgaat 360
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ccaaatcaag gtaacttgct cccttctgct acgggccttg gtcttggttt gtcctcacc 480
agtcggaact ccctaccact ttcaggagag tggtttttagg cccgtggggc tgttctgttc 540
caagcagtgt gagaacatgg ctggtagagg ctctagctgt gtgcgggggc tgaaggggag 600

005760-00999960

tgggttctcg cccaaagagc atctgcccac ttcccacctt cccttctccc accagaagct 660
tgcctgagct gtttggacaa aaatccaaac cccacttgge tactctggcc tggcttcagc 720
ttggaaccca atacctaggc ttacaggcca tcctgagcca ggggcctctg gaaattctct 780
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gagaccacac agctagacaa 20

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name ARNT_01
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name NMYC_01
score 0.965
sequence actcacgtgctg
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<221> protein_bind
<222> 193..204
<223> matinspector prediction
name USF_01
score 0.985
sequence actcacgtgctg
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<222> complement(193..204)

005750 00929950

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name USF_01
score 0.985
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score 0.956
sequence cagcacgtgagt
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name MYCMAX_02
score 0.972
sequence cagcacgtgagt
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<222> 195..202
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name USF_C
score 0.997
sequence tcacgtgc
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name USF_C
score 0.991
sequence gcacgtga
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<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga
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<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct
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<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc
<220>
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<222> complement(460..470)
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name AP1_Q4

005760-009E9960

score 0.963
sequence agtgactgaac
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<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac
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<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C
score 1.000
sequence tgtggtctc
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kawaagctca gcaccggtgc ccatacacagg gccggcagca cacacatccc attactcaga 180
aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta 240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaattcc aagtgattgt 300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag 360
gttgctctgc ccattggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc 420
cgtgtcttct gctgtctccc gctcacatcc cacacttgtg ttcagtcact gagttacaga 480
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tagctgtgtg gtctc 555

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ggccatacac ttgagtgc 19

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<222> 635..682
<223> homology
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 est

<220>
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<222> 625..1084
<223> homology
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 est

<220>
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<222> 779..1084
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<222> 144..506
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005760' 0099990

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<221> misc_feature
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 est
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<221> misc_feature
<222> 352..523
<223> homology
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<220>
<221> misc_feature
<222> 218..351
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<223> homology

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<222> 550..917
<223> homology
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cgacagcgcc ggcccctggg gcccgcaagt cgtcacagac gatgatggcc agggcccggg      120
ggctaaggac ggcagctcct ttagcggcag agttttccga gtgaccttct tg atg ctg      178
                                         Met Leu
gct gtt tct ctc acc gtt ccc ctg ctt gga gcc atg atg ctg ctg gaa      226
Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu
-10 -5 1 5
tct cct ata gat cca cag cct ctc agc ttc aaa gaa ccc ccg ctc ttg      274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
10 15 20
ctt ggt gtt ctg cat cca aat acg aag ctg cga cag gca gaa agg ctg      322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
25 30 35
ttt gaa aat caa ctt gtt gga ccg gag tcc ata gca cat att ggg gat      370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
40 45 50
gtg atg ttt act ggg aca gca gat ggc cgg gtc gta aaa ctt gaa aat      418
Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn
55 60 65
ggg gaa ata gag acc att gcc cgg ttt ggt tcg ggc cct tgc aaa acc      466
Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr
70 75 80 85
cga ggt gat gag cct gtg tgt ggg aga ccc ctg ggt atc cgt ggc agg      514
Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Gly Arg
90 95 100
gcc caa tgg gac tct ctt tgt ggc cga tgc ata caa agg gac tat ttg      562
Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp Tyr Leu
105 110 115
aag taaatccctg gaaacgtgaa gtgaaactgc tgcgtgcctc cgagacaccc      615
Lys
attgagggga agaacatgtc ctttgtgaat gatcttagag tcactcagga tgggaggaag      675
atattatttca ccgattctag cagcaaattg caaagacgag actacctgct tctggtgatg      735
gagggcacag atgacgggag cctgctggag tatgatactg tgaccagga agtaaaagtt      795
ttattggacc agctgcggtt cccgaatgga gtccagctgt ctccctgcaga agactttgtc      855
ctggtggcag aaacaacat ggccaggata cgaagagtct acgttttctg cctgatgaag      915
ggcggggctg atctgtttgt ggagaacatg cctggatttc cagacaacat ccggcccagc      975
agctctgggg ggtactgggt gggcatgtcg accatccgcc ctaaccctg gttttccatg      1035
ctggatttct tatctgagag accctggatt aaaaggatga tttttaangg taaaaaaaaa      1095
aaa
<210> 41
<211> 855
<212> DNA
<213> Homo sapiens
<220>
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0969360.091500

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<221> sig_peptide
<222> 267..371
<223> Von Heijne matrix
      score 5.90000009536743
      seq LCGLLHLWLKVFS/LK

<220>
<221> polyA_signal
<222> 817..822
<220>
<221> polyA_site
<222> 842..855
<220>
<221> misc_feature
<222> 608..811
<223> homology
      id :M85769
      est

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tcagtcagat actagtcaat atcaaatcat gtagatggcg gcatttttagg cctcggacac      120
catccctaca tgacagtgac aatgatgaac tctcctgtag aaaattatat aggagtataa      180
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa      240
gtagcagtggt ttcagcacac tttgggt atg ttg act gtt aat gat gta cgt ttc      293
                               Met Leu Thr Val Asn Asp Val Arg Phe
                               -35                               -30

tat aga aat gtc agg tcc aac cat ttc cca ttt gtt cga cta tgt ggt      341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
      -25                               -20                               -15

ctg tta cat tta tgg ctt aaa gtc ttt tct ctt aaa cag tta aaa aaa      389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
      -10                               -5                               1                               5

aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg      437
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
                               10                               15                               20

tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatgggtttat      485
Tyr Val Cys Val Phe Ile
      25

ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca      545
tattttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga      605
tattttctcta gttttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg      665
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt      725
cagagaagaa catttaaagg gttaatatatt ttgaaacggt ttcagataat atctatttga      785
ttattgtggc ttctatttga aatgtgtcta aaataaaatg ctgtttattt aaaatgaaaa      845
aaaaaaaaaa                                     855

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<222> 174..266
<223> Von Heijne matrix
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<222> 1144..1149
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<220>
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<222> 1165..1176
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<221> misc_feature
<222> 886..1134
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<220>
<221> misc_feature
<222> 756..894
<223> homology
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<220>
<221> misc_feature
<222> 655..755
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 est
<220>
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<222> 167..367
<223> homology
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<222> 66..172
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 est
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<222> 3..338
<223> homology
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<221> misc_feature
<222> 334..374
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 est
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<223> homology
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      est
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<222> 756..894
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<221> misc_feature
<222> 590,601
<223> n=a, g, c or t
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aacaagccaa ggagccaaga cgagagggac acacggacaa acaacagaca gaagacgtac      120
tggccgctgg actccgctgc ctcccccatc tccccgccat ctgcgcccgg agg atg      176
                                     Met
agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc tcc      224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                               -25                -20                -15
ttc tgg agc cct ttg tcc acc agg tcg ggg ggc act cat gcg tgc tcc      272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
                               -10                -5                1
gct tca atg aga caa ccc tgg gca agc ccc tgg tcc caa ggg aac atc      320
Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn Ile
                               5                10                15
agt tct acg aga ccc tcc ctg ctg aga tgc gca aat tct ctc ccc agt      368
Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro Ser
                               20                25                30
aca aag gac aaa gcc aaa ggc ccc ttg tta gct ggc cat ccc tgc ccc      416
Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys Pro
35                               40                45                50
att ttt tcc cct ggt cct ttc ccc tgt ggc cac agg gaa gtg tgg cct      464
Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp Pro
                               55                60                65
gaa tac ccc acc ccg gct cct ctg cac cca gag ctg ggg gcc acc tca      512
Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr Ser
                               70                75                80
gaa gtg tca tct ctc tct gag cac gsa ttc ccc tgc agc agt cga gga      560
Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg Gly
                               85                90                95
ctg agc aga ttg agt gat gct ggg gca gan adg cct gag ang aaa ggt      608
Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys Gly
100                               105                110
gtt cag cca gtc gtt tgt aag gcg ctc gkc ggm act gct gaa acg ccc      656
Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr Pro
115                               120                125                130
cca ccc tgacagcccc atcctcaaag actgtcttaa ttactcatgg caggttctag      712
Pro Pro
agacttaagg ggaaaagctg ctttcaaggc caccacatgt ctggtgctcc ccmaccagst      772
statctgcct wgtgttcatt ttgytatttt gtgasgtgag acagcaaaga ccaataaaaa      832
catattttat aagaacaaaa ggcytgggtg cctacccgkg tgggggcacw gtgggaagcc      892
ttctgmtagg gtgtcttgtg ctgtrtggyt tgttttgttt gcccyyttat tttgctttgc      952
ttaccagtc ttcccytamt yttggatgst tyttaaccct caggcaaac tgtgttcccc      1012
ctgtattcag gstytgcttt aaagcaagcc atgaggctgt tggagtttct gtttagggca      1072
ttaaaaattc ccgcaaacta taaagagcaa tgttttcagt yttttaggat tagaagaatt      1132
acataaaaat taataaacat tttcaatgat ggaaaaaaa aaaa      1176

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seq FSFMLLGMGGCLP/GF

<220>
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<222> 614..619
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<222> 635..648
<400> 43

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tccttagagt	tctccctcca	ttagtagttg	tcttagggtc	tgtttctggg	gagccctgcc	120
taagactcat	gctacaagaa	gttaaataag	tttcccgaag	tcacacagct	agcctctcat	180
cccttttcta	ctgagaggaa	gtggaatgca	ctccgacaag	gataagggtt	tattgtgagc	240
tggccttgga	attaaaccac	caccaacaca	cttttggatt	atcagaaggt	ggaaggagt	300
caaatgccag	ttacggtgat	gcgttcaaca	tccttatttc	cagtctttat	gacgcctttc	360
ctgaatcaca	ggtgcattgg	ggtgcttctc	cctccccagg	actcccaccc	aactttgtga	420
acacaacca	cttagaggag	ttatttcagc	acattatga	atg ttg ggg	acc acg	474

Met Leu Gly Thr Thr

-30

ggc	ctc	ggg	aca	cag	ggt	cct	tcc	cag	cag	gct	ctg	ggc	ttt	ttc	tcc	522
Gly	Leu	Gly	Thr	Gln	Gly	Pro	Ser	Gln	Gln	Ala	Leu	Gly	Phe	Phe	Ser	

-25

-20

-15

ttt	atg	tta	ctt	gga	atg	ggc	ggg	tgc	ctg	cct	gga	ttc	ctg	cta	cag	570
Phe	Met	Leu	Leu	Gly	Met	Gly	Gly	Cys	Leu	Pro	Gly	Phe	Leu	Leu	Gln	

-10

-5

1

5

cct	ccc	aat	cga	tct	cct	act	ttg	cct	gca	tcc	acc	ttt	gcc	cat	615
Pro	Pro	Asn	Arg	Ser	Pro	Thr	Leu	Pro	Ala	Ser	Thr	Phe	Ala	His	

10

15

20

taaagtcaat	tctccacca	taaaaaaaa	aaa	648
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<212> DNA
<213> Homo sapiens
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<222> 79..369
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seq RLPLVVSFIASSS/AN

<220>
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<221> polyA_site
<222> 1240..1251
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<222> 2..423
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est
<220>
<221> misc_feature
<222> 463..520
<223> homology
id :AA056667
est
<220>
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<222> 418..467
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gagagaaggg gggtcatc atg gcg gat gac cta aag cga ttc ttg tat aaa 111
                Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys
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aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga 159
Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg
-85                                -80                                -75

gat gga gta cct gtt att aaa gtg gca aat gac aat gct cca gag cat 207
Asp Gly Val Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His
-70                                -65                                -60                                -55

gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa 255
Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln
-50                                -45                                -40

gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat 303
Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr
-35                                -30                                -25

aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt 351
Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser
-20                                -15                                -10

ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc cta gaa 399
Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu
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aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa att 447
Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile
15                                20                                25

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Ser

atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct caagaaaggg 560
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ggagcagtcct ctgaagacgc ttctactgag aggtctgcc atg gcc tct ctt ggc 174
Met Ala Ser Leu Gly
-20

ctc caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca 222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
-15 -10 -5

ctg gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt 270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly
1 5 10

gcc agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa 318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu
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tgt gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc 366
Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr

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	aca	tcc	agt	gca	atc	tcc	tcc	ctg	gcc	tgc	att	atc	tct	gtg	gtg	ggc	462
	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	
				65				70						75			
	atg	ara	tgc	aca	gtc	ttc	tgc	cag	gaa	tcc	cga	gcc	aaa	gac	aga	gtg	510
	Met	Xaa	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	
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	gcg	gta	gca	ggg	gga	gtc	ttt	ttc	atc	ctt	gga	ggc	ctc	ctg	gga	ttc	558
	Ala	Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	
		95				100					105						
	att	cct	gtt	gcc	tgg	aat	ctt	cat	ggg	atc	cta	cgg	gac	ttc	tac	tca	606
	Ile	Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	
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	cca	ctg	gtg	cct	gac	agc	atg	aaa	ttt	gag	att	gga	gag	gct	ctt	tac	654
	Pro	Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	
				130						135				140			
	ttg	ggc	att	att	tct	tcc	ctg	ttc	tcc	ctg	ata	gct	gga	atc	atc	ctc	702
	Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	Leu	
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	tgc	ttt	tcc	tgc	tca	tcc	cag	aga	aat	cgc	tcc	aac	tac	tac	gat	gcc	750
	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	Asp	Ala	
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	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	Pro	Gly	Gln	
		175				180					185						
	cct	ccc	aaa	gtc	aag	agt	gag	ttc	aat	tcc	tac	agc	ctg	aca	ggg	tat	846
	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser	Leu	Thr	Gly	Tyr	
	190				195				200				205				
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	Val																
	tggacagcac	cccagaggcc	acagggtgagg	gacactacca	ctggatcgtg	tcagaagggtg											959
	ctgctgaggg	tagactgact	ttggccattg	gattgagcaa	aggcagaaat	gggggctagt											1019
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	aacctamtty	tcaagcttcc	ctccaaagaa	amtgattggc	cctggaacct	ccatcccact											1379
	yttgttatga	ctccacagtg	tccagamtaa	tttgtgcatg	aactgaaata	aaaccatcct											1439
	acggatatyca	gggaacagaa	agcaggatgc	aggatgggag	gacaggaagg	cagcctggga											1499
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                                         Met Phe Ala Pro
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gcg gtg atg cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc 165
Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
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ccc atg ttg ttg ctg att gtt gga ggt tct ttt ggt ctt cgt gag ttt 213
Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe
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tct caa atc cga tat gat gct gtg aag agt aaa atg gat cct gag ctt 261
Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu
5                      10                      15                      20

gaa aaa aaa ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag 309
Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu
      25                      30                      35

gga agt atc tgt tgaagggcta ctatctttcc ttggcccttc tcccttgttg 361
Gly Ser Ile Cys
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ttgggaaaat caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt 481
gggaagatcc tgacctctc caaggaagaa atccaggaaa gccttaagac taagacaact 541
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005160-009990

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atg aac ach ttt gag cca gac agc ctg gct gtc att gct ttc ttc ctc 406
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Pro Ile Trp Thr Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro
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cca tcc acc agt cta ttt att aac tta gca aga gga caa ata aag ggc 502
Pro Ser Thr Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly
1 5 10
cct ctt ggc ttg att ttg ctt ctt tct ttc tgt gga gga tat act aag 550
Pro Leu Gly Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys
15 20 25
tgc gac ttt gcc cta tcc tat ttg gaa atc cct aac aga att gag ttt 598
Cys Asp Phe Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe
30 35 40
tct att atg gat cca aaa aga aaa aca aaa tgc taatgaagcc atcasgtcaa 651
Ser Ile Met Asp Pro Lys Arg Lys Thr Lys Cys
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gtgagctgct gagatttggg agtctgcgct aggcccgtt ggagttctga gccgatggaa 180
gagttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac 229
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
-30 -25 -20
aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt 277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
-15 -10 -5
tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag 325
Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys
1 5 10
ggt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata 373
Gly Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile
15 20 25
tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac 421
Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp
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tgg aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc 469
Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu
50 55 60
caa gga aga aat cca gaa agc ctt aag act aag aca act tgactctgct 518
Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65 70
gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt cctaatatat 578
acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg ggtaatttgg 638
atggacaaaa ktaatctkct actaaaggtc atgtaccagg tttttatact tcccagctaa 698
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aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt 357
                                         Met Trp Trp Phe
                                         -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
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gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa 501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
      20                      25                      30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc att 549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Ile
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gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct gaa 597
Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro Glu
      50                      55                      60
gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga ata 645
Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly Ile
      65                      70                      75
ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag gaa aac aac 693
Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Glu Asn Asn
      80                      85                      90                      95
cct ttt tgc tgc aca tgt aag tgg agc tgt gct tac ctt tgg tat ggg 741
Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr Leu Trp Tyr Gly
      100                      105                      110
ctc att ata tat gtt tgt tca gac cat cct ttc cta cca aaa tgc agc 789
Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu Pro Lys Cys Ser
      115                      120                      125
cca aaa tcc aat ggc aaa aca agt ctt ctg gat cag act gtt gtt ggt 837
Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln Thr Val Val Gly
      130                      135                      140
tat ctg gtg tgg agt aag tgc act tagcatgctg acttgctcat cagttttgca 891
Tyr Leu Val Trp Ser Lys Cys Thr
      145                      150
cagtggcaat tttgggactg atttagaaca gaaactccat tggaacccccg aggacaaagg 951
ttatgcgctt cacatgatca ctactgcagc agaatgggtct atgtcattttt ccttcttttg 1011
ttttttcctg acttacattc gtgatttttca gaaaattttcc ttacgggttg aagccaactt 1071
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aanccactta antcaaggct gacagstaac acgtgatgaa tgctgataat caggaaacat 1311
gaaagaagcc atttgcatag attattytaa aggatatcat caagaagamt attaaaaaca 1371
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tgrsagtgtta mtggattatt ccttgggact gaatgacttg aatgtttccc cgcctgagct 180

aacagtccat gtgggtgatt cagctctgat ggg atg tgt ttt cca gag cac aga 234

Met Cys Phe Pro Glu His Arg

-40

aga caa atg tat att caa gat aga ctg gac tct gtc acc agg aga gca 282

Arg Gln Met Tyr Ile Gln Asp Arg Leu Asp Ser Val Thr Arg Arg Ala

-35 -30 -25 -20

cgc caa gga cga ata tgt gct ata cta tta ctc caa tct cag tgt gcc 330

Arg Gln Gly Arg Ile Cys Ala Ile Leu Leu Leu Gln Ser Gln Cys Ala

-15 -10 -5

tat tgg gcg ctt cca gaa ccg cgt aca ctt gat ggg gga cat ctt atg 378

Tyr Trp Ala Leu Pro Glu Pro Arg Thr Leu Asp Gly Gly His Leu Met

1 5 10

caa tgatggctct ctctgctcc aagatgtgca agaggctgac cagggaaacct 431

Gln

atatctgtga aatccgcctc aaaggggaga gccaggtgtt caagaaggcg gtgggtactgc 491

atgtgcttcc agaggagccc aaaggtacgc aaatgcttac ttaaagaggg gccaaggggc 551

aagagctttc atgtgcaaga ggcaaggaaa ctgattatct tgagtaaata ccagcctttg 611

ggctaagtac ttaccacaga gtgaatcttc aaagaaatga ntcattaaat tatttcagrt 671

cagaataaaa atakgagtta ttttagttaa kaataaaaata ttgataatta ttgtattatt 731

actttaaaaca cacttcccc tcacaaaagc cctgtgaagg atgttttggt cacatataat 791

gtccaaatat gttttggaca catatttatt aaatgggaata aatagtamtt gaaccctggc 851

accthtgaca acaaagtcya tgtyttttt actatgccct aataccttts atcagttatc 911

cacattgatg ctacatygtt attttatagg taccctatgt taggtgtttt gggggataga 971

aaagaaataa gcagkycagg ctgagtggt catgcctgta atcctagcat tttgggaggc 1031

tgaggcagca gaamtgcctg agccccagg ttcaagactg cagttagcta tgawggcacc 1091

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gtcggctttc ttggtgcctt ggttcacccc taagggtcct aaccggggag ttatcattac 180
catgttggtg acctgttcag tttgctgcta tctcttttgg ctgattgcaa ttctggccca 240
actcaaccct ctctttggac cgcaattgaa aaatgaaacc atctgggtatc tgaagtatca 300
ttggccttga ggaagaagac atgctctaca gtgctcagtc tttgagggtca cgagaagaga 360
atgccttcta g atg caa aat cac ctc caa acc aga cca ctt ttc ttg act 410
Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr
-20 -15 -10
tgc ctg ttt tgg cca tta gct gcc tta aac gtt aac agc aca ttt gaa 458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
-5 1 5
tgc ctt att cta caa tgc agc gtg ttt tcc ttt gcc ttt ttt gca ctt 506
Cys Leu Ile Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu
10 15 20
tgg tgaattacgt gcctccataa cctgaactgt gccgactcca caaaacgatt 559
Trp
atgtactctt ctgagataga agatgctggt cttctgagag atacgttact ctctccttgg 619
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cgcccgtgac c atg tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg 170
Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
-25 -20
cgg gtg ccc ttg tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc 218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15 -10 -5 1
gta aag aca ctg ctc cca gta cca agt ttt gaa gat gtt tcc att cct 266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
5 10 15
gaa aaa ccc aag ctt aga ttt att gaa agg gca cca ctt gtg cca aaa 314
Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys
20 25 30
gta aga aga gaa cct aaa aat tta agt gac ata cgg gga cct tcc act 362
Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr
35 40 45
gaa gct acg gag kkk aca gaa ggc aat ttt gca atc ttg gca ttg ggt 410
Glu Ala Thr Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly
50 55 60 65
ggg ggc tac ctg cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc 458
Gly Gly Tyr Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile
70 75 80
aac cgc tct atg gac ccc aag aac atg ttt gcc ata tgg cga gta cca 506
Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro
85 90 95
gcc cct ttc aag ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg 554
Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly
100 105 110
gga ggc aaa ggt gct att gac cac tac gtg aca cct gtg aag gct ggc 602
Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly
115 120 125
cgc mww gww gta gag atg ggt ggg cgt tgt gma ttt gaa gaa gtg caa 650
Arg Xaa Xaa Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln
130 135 140 145
ggg ttc ctt gac cag gtt gcc cac aag ttg ccc tty gca gca aag gct 698
Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala
150 155 160
gtg agc cgc ggg act yta gag aag atg cga aaa gat caa gag gaa aga 746
Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg
165 170 175
gaa mgt aac aac cag aac ccc tgg aca ttt gag cga ata gcc act gcc 794
Glu Xaa Asn Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala
180 185 190
mac atg ctg ggc ata cgg aaa gta ctg agc cca tat gac ttg acc cac 842
Xaa Met Leu Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His
195 200 205
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Lys Gly Lys Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val
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<222> 425..488
<223> homology
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      est
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<222> 52..195
<223> homology
      id :W38899
      est
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<222> 197..324
<223> homology
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      est
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<222> 443..477
<223> homology
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      est
<220>
<221> misc_feature
<222> 197..338
<223> homology
      id :W52820
      est
<220>
<221> misc_feature
<222> 71..195

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09663600 091500

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<223> homology
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      est
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<221> misc_feature
<222> 339..401
<223> homology
      id :W52820
      est
<220>
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<222> 425..469
<223> homology
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      est
<220>
<221> misc_feature
<222> 40..195
<223> homology
      id :W19506
      est
<220>
<221> misc_feature
<222> 9..10,12
<223> n=a, g, c or t
<400> 53
agagctgtnn cnsaagtagg ggagggcggg gctccgcmgm ggtggcggdh tgctatcgct      60
tcgcagaacc tactcaggca gccagctgag aagagttgag ggaaagtgct gctgctgggt      120
ctgcagacgc gatggataac gtgcagccga aaataaaaaca tcgccccttc tgcttcagtg      180
tgaaaggcca cgtgayag atg ctg cgg ctg gat att atc aac tca ctg gta      231
                    Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
                    -30                    -25                    -20
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa      279
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
                    -15                    -10                    -5
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca      327
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
                    1                    5                    10
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc      375
Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe
                    15                    20                    25
aat ccc agc ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa      423
Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
30                    35                    40                    45
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa catatttctg      479
Val Leu
tattcttcca aaaaaaaaaa a      500

<210> 54
<211> 765
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 293..385
<223> Von Heijne matrix
      score 4.40000009536743
      seq TCCHLGLPHPVRA/PR
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005T60-0099960

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<221> polyA_signal
<222> 733..738
<220>
<221> polyA_site
<222> 752..765
<220>
<221> misc_feature
<222> 310..576
<223> homology
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      est
<220>
<221> misc_feature
<222> 119
<223> n=a, g, c or t
<400> 54
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tgagggggcga gggaaaagtt ttcctcaggt gtggtgggga gagggaggcg gatgccgng      120
aaaccgtagg kacgcggtca gaaaggcgac gggctgtcgg agttggaaag ggacgcctgg      180
tttcccccca agcgaaccgg gatgggaagt gacttcaatg agattgaact tcagctggat      240
tgaaagagag gctagaagtt cggcttgcca gcagcctcct tagtagagcg ga atg agt      298
                                         Met Ser
                                         -30
aat acc cac acg gtg ctt gtc tca ctt ccc cat ccg cac ccg gcc ctc      346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu
          -25                      -20                      -15
acc tgc tgt cac ctc ggc ctc cca cac ccg gtc cgc gct ccc cgc cct      394
Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro Arg Pro
          -10                      -5                      1
ctt cct cgc gta gaa ccg tgg gat cct agg tgg cag gac tca gag cta      442
Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser Glu Leu
          5                      10                      15
agg tat cca cag gcc atg aat tcc ttc cta aat gag cgg tca tcg ccg      490
Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser Ser Pro
          20                      25                      30                      35
tgc agg acc tta agg caa gaa gca tcg gct gac aga tgt gat ctc      535
Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp Leu
          40                      45                      50
tgaacctgat agattgctga ttttatctta ttttatcctt gacttggtac aagttttggg      595
atttctgaaa agaccataca gataaccaca aatatcaaga aagtcgtctt cagtattaag      655
tagaatttag atttaggttt ccttcctgct tcccacctcc ttcgaataag gaaacgtctt      715
tgggaccaac tttatggaat aaataagctg agctgcaaaa waaaaaaaaa      765

<210> 55
<211> 584
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 130..189
<223> Von Heijne matrix
      score 3.5
      seq KFCLICLLTFIFH/HC
<220>
<221> polyA_signal
<222> 546..551
<220>
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005150-00959360

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<221> polyA_site
<222> 572..584
<400> 55
aagacgcgcc gggtttctgcg acgcagtttag cgcagtctgc tttggtgaat acacgatttg      60
gtgcagccgg gggtttggtac cgagcggaga ggagatgcac acggcactcg agtgtgagga      120
aaaatagaa atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt ttg      171
      Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu
      -20 -15 -10
ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat gac      219
Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp
      -5 1 5 10
cat ggc cct gaa gag ctt cac aga cag cat cgt gga atg aca gaa ttg      267
His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu
      15 20 25
gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa tac      315
Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr
      30 35 40
tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta tcc      363
Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser
      45 50 55
ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag aga      411
Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg
      60 65 70
aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt tct      459
Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser
      75 80 85 90
cat tta agg tat ttt ggc agt tca aga ggg aaa gca ttt tca ctc aca      507
His Leu Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
      95 100 105
taaccaccca gcattcccat aatcatttaa attcagaaaa tcaaaactgt gaccagtgt      567
wtccacaaaa aaaaaaa      584

<210> 56
<211> 1387
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 191..325
<223> Von Heijne matrix
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      seq VLVYLVTAERVWS/DD

<220>
<221> polyA_signal
<222> 1348..1353
<220>
<221> polyA_site
<222> 1374..1387
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
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      est

<220>
<221> misc_feature
<222> 791..887
<223> homology
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005T60:009E9960

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est
<220>
<221> misc_feature
<222> 94..524
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est
<220>
<221> misc_feature
<222> 44..94
<223> homology
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est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
id :AA236941
est
<220>
<221> misc_feature
<222> 935..1279
<223> homology
id :AA480326
est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
id :AA480326
est
<220>
<221> misc_feature
<222> 724..1148
<223> homology
id :AA234245
est
<220>
<221> misc_feature
<222> 944..1279
<223> homology
id :AA479344
est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
id :AA479344
est
<220>
<221> misc_feature
<222> 1070..1212
<223> homology
id :AA133636
est
<220>
<221> misc_feature

005760:009E9960

<222> 1258..1372
<223> homology
id :AA133636
est

<220>
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<222> 938..1054
<223> homology
id :AA133636
est

<220>
<221> misc_feature
<222> 94..436
<223> homology
id :AA133635
est

<220>
<221> misc_feature
<222> 32..94
<223> homology
id :AA133635
est

<220>
<221> misc_feature
<222> 895..1273
<223> homology
id :AA479453
est

<220>
<221> misc_feature
<222> 1258..1371
<223> homology
id :AA253214
est

<220>
<221> misc_feature
<222> 94..268
<223> homology
id :AA482378
est

<220>
<221> misc_feature
<222> 946
<223> n=a, g, c or t
<400> 56

actcccaggc	tgggccagca	cacccggcag	gctctgtcct	ggaaacaggc	ttcaacgggc	60
ttccccgaaa	accttccccg	cttctggata	tgaavattca	agctgcttgc	tgagtcctat	120
tgccggctgc	tgggagccag	gagagccctg	aggagtagtc	aetcagtagc	agctgacgcg	180
tgggtccacc	atg aac tgg	agt atc ttt	gag gga ctc	ctg agt ggg	gtc	229
	Met Asn Trp	Ser Ile Phe	Glu Gly Leu	Leu Ser Gly	Val	
	-45		-40		-35	
aac aag tac	tcc aca gcc	ttt ggg	cgc atc tgg	ctg tct ctg	gtc ttc	277
Asn Lys Tyr	Ser Thr Ala	Phe Gly Arg	Ile Trp Leu	Ser Leu Val	Phe	
	-30		-25		-20	
atc ttc cgc	gtg ctg gtg	tac ctg	gtg acg gcc	gag cgt gtg	tgg agt	325
Ile Phe Arg	Val Leu Val	Tyr Leu	Val Thr Ala	Glu Arg Val	Trp Ser	
	-15		-10		-5	
gat gac cac	aag gac ttc	gac tgc	aat act cgc	cag ccc ggc	tgc tcc	373

005160-00999960

Asp 1	Asp	His	Lys	Asp 5	Phe	Asp	Cys	Asn	Thr 10	Arg	Gln	Pro	Gly	Cys 15	Ser	
aac	gtc	tgc	ttt	gat	gag	ttc	ttc	cct	gtg	tcc	cat	gtg	cgc	ctc	tgg	421
Asn	Val	Cys	Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	
			20					25					30			
gcc	ctg	cag	ctt	atc	ctg	gtg	aca	tgc	ccc	tca	ctg	ctc	gtg	gtc	atg	469
Ala	Leu	Gln	Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	
		35					40					45				
cac	gtg	gcc	tac	cgg	gag	gtt	cag	gag	aag	agg	cac	cga	gaa	gcc	cat	517
His	Val	Ala	Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	
	50					55				60						
ggg	gag	aac	agt	ggg	cgc	ctc	tac	ctg	aac	ccc	ggc	aag	aar	cgg	ggg	565
Gly	Glu	Asn	Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	
65				70					75					80		
ggg	ctc	tgg	tgg	aca	tat	gtc	tgc	agc	cta	gtg	ttc	aag	gcg	agc	gtg	613
Gly	Leu	Trp	Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	
				85				90					95			
gac	atc	gcc	ttt	ctc	tat	gtg	ttc	cac	tca	ttc	tac	ccc	aaa	tat	atc	661
Asp	Ile	Ala	Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	
		100					105					110				
ctc	cct	cct	gtg	gtc	aag	tgc	cac	gca	gat	cca	tgt	ccc	aat	ata	gtg	709
Leu	Pro	Pro	Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	
		115				120						125				
gac	tgc	ttc	atc	tcc	aag	ccc	tca	gag	aag	aac	att	ttc	acc	ctc	ttc	757
Asp	Cys	Phe	Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	
	130					135				140						
atg	gtg	gcc	aca	gct	gcc	atc	tgc	atc	ctg	ctc	aac	ctc	gtg	gag	ctc	805
Met	Val	Ala	Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	
145				150				155						160		
atc	tac	ctg	gtg	agc	aag	aga	tgc	cac	gag	tgc	ctg	gca	gca	agg	aaa	853
Ile	Tyr	Leu	Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	
				165				170					175			
gct	caa	gcc	atg	kgc	aca	ggt	cat	cac	ccc	cav	gat	acc	acy	ttt	tcc	901
Ala	Gln	Ala	Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser	
		180					185					190				
kgc	aaa	caa	gas	gac	ytic	ytt	tgc	ggk	gac	ytic	atc	ttt	ctg	ggn	tca	949
Xaa	Lys	Gln	Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser	
		195					200					205				
gac	agt	cat	cyt	cct	ytic	tta	cca	gac	cgc	ccc	cga	gac	cat	gtg	aag	997
Asp	Ser	His	Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	
	210					215				220						
aaa	acc	aty	ttg	tgagggg	ctg	cctgg	amtgg	tytgg	caggt	tgggc	cctgga					1049
Lys	Thr	Ile	Leu													
225																
tgaggaggct	ytagcaty	tyt	tcataggtgc	aacctgagag	tgaggaggagct	aagccatgag										1109
gtaggggcag	gcaagagaga	ggattcagac	gytytgggag	ccagttccta	gtcctcaamt											1169
ccagccacct	gccccagsth	gacggcamtg	ggccagttcc	ccctygtgsty	tgcagstcgg											1229
tttcctttty	tagaatggaa	atagtggagg	ccaatgccca	gggttgagg	gaggaggcg											1289
ttcatagaag	aacacacatg	cgggcacctt	catygtgtgt	ggccactgt	cagaacttaa											1349
taaaagtcaa	mtcatttgct	ggttaaaaaa	aaaaaaaa													1387

<210> 57
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 <213> Homo sapiens
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 <221> sig_peptide
 <222> 141..251

005160-00929950

<223> Von Heijne matrix
score 4
seq PLSLDCGHS LCRA/CI

<220>

<221> polyA_signal

<222> 1354..1359

<220>

<221> polyA_site

<222> 1375..1385

<220>

<221> misc_feature

<222> 1183..1240

<223> homology

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est

<220>

<221> misc_feature

<222> 176..239

<223> homology

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est

<220>

<221> misc_feature

<222> 803..854

<223> homology

id :AA286417

est

<220>

<221> misc_feature

<222> 1183..1213

<223> homology

id :AA608077

est

<400> 57

aacacccacc ctggcttttc ttcacctctt caaccaggag ccgagatttc tggtgctctg 60

aagccatcca ggggtcttta accagaagag agaggagagc ctcaggagtt aggaccagaa 120

gaagccaggg aagcagtgc a atg gct tca aaa atc ttg ctt aac gta caa gag 173

Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu

-35

-30

gag gtg acc tgt ccc atc tgc ctg gag ctg ttg aca gaa ccc ttg agt 221

Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser

-25

-20

-15

cta gac tgt ggc cac agc ctc tgc cga gcc tgc atc act gtg agc aac 269

Leu Asp Cys Gly His Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn

-10

-5

1

5

aag gag gca gtg acc agc atg gga gga aaa agc agc tgt cct gtg tgt 317

Lys Glu Ala Val Thr Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys

10

15

20

ggg atc agt tac tca ttt gaa cat cta cag gct aat cag cat cgg gcc 365

Gly Ile Ser Tyr Ser Phe Glu His Leu Gln Ala Asn Gln His Arg Ala

25

30

35

aac ata gtg gag aga ctc aag gag gtc aag ttg agc cca gac aat ggg 413

Asn Ile Val Glu Arg Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly

40

45

50

aag aag aga gat ctc tgt gat cat cat gga gag aaa ctc cta ctc ttc 461

Lys Lys Arg Asp Leu Cys Asp His His Gly Glu Lys Leu Leu Leu Phe

55

60

65

70

tgt aag gag gat agg aaa gtc att tgc tgg ctt tgt gag cgg tct cag 509

005160-0096960

Cys Lys Glu Asp Arg Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln
75 80 85
gag cac cgt ggt cac cac aca ggt cct cac gga gga agt att caa gga 557
Glu His Arg Gly His His Thr Gly Pro His Gly Gly Ser Ile Gln Gly
90 95 100
atg tca gga gaa act cca ggc agt cct caa gag gct gaa gaa gga aga 605
Met Ser Gly Glu Thr Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg
105 110 115
gga gga agc tgagaagctg gaagctgaca tcagagaaga gaaaacttcc 654
Gly Gly Ser
120
tggaagtatc aggtacaaac tgagagacaa aggatacaaa cagaatttga tcagcttaga 714
agcatcctaa ataatgagga gcagagagag ctgcaaagat tggaagaaga agaaaagaag 774
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atgagtggaa tcatgaaatg gagtgagatc tggaggctga aaaagccaaa aatgggtttcc 954
aagaaactga agactgtatt ccatgctcca gatctgagta ggatgctgcr aatgtttaga 1014
ggaactgaca gctgtccggg gctactgggt ggatgtcaca ctgaattcag tcaacctaaa 1074
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tcagtgttat aattatggtg tktttgggat cccaatattt btcctsstgg gaaacattac 1194
tgggaagtgg acgtgtccaa gaaaactgcc tggatcctgg ggggtatactg tagaacatat 1254
tcccgccata tgaagtatgt tgttagaaga tgtgcaaaty gtcaaaatbt ttacaccaaa 1314
tacagacctc tatttggsta ctgggttata ggggttacaga ataaatgtaa gtatggtgcc 1374
aaaaaaaaa a 1385

<210> 58
<211> 1497
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 212..268
<223> Von Heijne matrix
score 8.60000038146973
seq LLWLALACSPVHT/TL
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<222> 1465..1470
<220>
<221> polyA_site
<222> 1489..1497
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<222> 958..1110
<223> homology
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est
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<222> 1202..1312
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id :W72124

005T60:009E9960

est
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<222> 1115..1190
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<222> 653..807

005150.0099990

<223> homology
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est

<220>

<221> misc_feature

<222> 907..1046

<223> homology
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est

<220>

<221> misc_feature

<222> 475..605

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<220>

<221> misc_feature

<222> 598..639

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<222> 1069..1190

<223> homology
id :AA181149
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<220>

<221> misc_feature

<222> 1362..1475

<223> homology
id :AA181149
est

<220>

<221> misc_feature

<222> 1202..1312

<223> homology
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est

<220>

<221> misc_feature

<222> 1312..1370

<223> homology
id :AA181149
est

<220>

<221> misc_feature

<222> 72,93

<223> n=a, g, c or t

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gcagatttcc anssagaaga cagagaagga gcnagtgggc atggaatggg ctgggggtcaa 120
agactgggtg cctgggagct gaggcagcca ccgtttcagc ctggccagcc ctctggaccc 180
cgaggttgga ccctactgtg acacacctac c atg cgg aca ctc ttc aac ctc 232

Met Arg Thr Leu Phe Asn Leu

-15

ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag 280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys

-10	-5	1	
tca gat gcc asa aaa ccg cct caa aga cgc tgc tgg aga aga gtc agt			328
Ser Asp Ala Xaa Lys Pro Pro Gln Arg Arg Cys Trp Arg Arg Val Ser			
5	10	15	20
ttt cag ata agc cgg tgc aar acc ggg gtt tgg tgg tgacggacct			374
Phe Gln Ile Ser Arg Cys Lys Thr Gly Val Trp Trp			
25	30		
caaagctgag agtgtggttc ttgagcatcg cagctactgc tcggcaaagg cccgggacag			434
acactttgct ggggatgtac tgggctatgt cactccatgg aacagccatg gctacgatgt			494
caccaaggtc tttgggagca agttcacaca gatctcaccg gtctggctgc agttgaagag			554
acgtggccgt gagatgtttg aggtcacggg cctccacgac gtggaccaag ggtggatgcg			614
agctgtcagg aagcatgccg agggcctgca catagtgcct cggctcctgt ttgaggactg			674
gacttacgat gatttccgga acgtcttaga cagtgaggat gagatagagg agctgagcaa			734
gaccgtggtc caggtggcaa agaaccagca ttctgatggc ttctgtggtg aggtctggaa			794
ccagctgcta agccagaagc gcgtgggcct catccacatg ctcacccact tggccgaggc			854
cctgcaccag gcccggtgc tggccctcct ggtcatcccg cctgccatca ccccgggac			914
cgaccagctg ggcattgtca agcacaagga gtttgagcag ctggcccccg tgctggatgg			974
tttcagcctc atgacctacg actactctac agcgcatcag cctggcccta atgcaccct			1034
gtcctggggt cgagcctgcg tccaggtcct ggaccggaa gtccaagtgg cgaagcaaaa			1094
tcctcctggg gctcaacttc tatgggtatgg actacgcgac ctccaaggat gcccgtagc			1154
ctgttgctcg ggcaggtac atccagacac tgaadggacc acaggccccg ggaatggtgt			1214
gggacagcca ggcctcagag cacttcttcg agtacaagaa gagccgcagt gggaggcacg			1274
tcgtcttcta cccaaccctg aagtccttcg aggtgcgggc tggagctggc ccgggagctg			1334
ggcgttgggg tctctatytg ggagctgggc cagggcctgg actacttyta cgacctgcty			1394
taggtgggca ttgcggcctc cgcggtggac gtgttytttt ytaagccatg gagtgagtga			1454
gcaggtgtga aatacaggcc tccactcctg ttgcaaaaaa aaa			1497

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005760-009E9960

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agggtaggga cttctcccg c agcgacgcgg ctggcaagac tgtttgtgtt gcgggggccc 120
gaacttcaag gtgattttac aacgag atg ctg ctc tcc ata ggg atg ctc atg 173
Met Leu Leu Ser Ile Gly Met Leu Met

-30

ctg tca gcc aca caa gtc tac acc atc ttg act gtc cag ctc ttt gca 221

005160' 009E9560

Leu	Ser	Ala	Thr	Gln	Val	Tyr	Thr	Ile	Leu	Thr	Val	Gln	Leu	Phe	Ala	
-25					-20					-15					-10	
ttc	tta	aac	cta	ctg	cct	gta	gaa	gca	gac	att	tta	gca	tat	aac	ttt	269
Phe	Leu	Asn	Leu	Leu	Pro	Val	Glu	Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	
				-5				1				5				
gaa	aat	gca	tct	cag	aca	ttt	gat	gac	ctc	ccc	gca	ara	ttt	ggt	tat	317
Glu	Asn	Ala	Ser	Gln	Thr	Phe	Asp	Asp	Leu	Pro	Ala	Xaa	Phe	Gly	Tyr	
		10					15				20					
aga	ctt	cca	gct	gaa	ggt	tta	aag	ggt	ttt	tta	att	aac	tca	aaa	cca	365
Arg	Leu	Pro	Ala	Glu	Gly	Leu	Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	
	25					30				35						
gag	aat	gcc	tgt	gaa	ccc	ata	gtg	cct	cca	cca	gta	aaa	gac	aat	tca	413
Glu	Asn	Ala	Cys	Glu	Pro	Ile	Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	
40				45				50						55		
tct	ggc	act	ttc	atc	gtg	tta	att	ara	ara	ctt	gat	tgt	aat	ttt	gat	461
Ser	Gly	Thr	Phe	Ile	Val	Leu	Ile	Xaa	Xaa	Leu	Asp	Cys	Asn	Phe	Asp	
				60				65						70		
ata	aag	ggt	tta	aat	gca	cag	aga	gca	gga	tac	aag	gca	gcc	ata	ggt	509
Ile	Lys	Val	Leu	Asn	Ala	Gln	Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	
		75				80						85				
cac	aat	ggt	gat	tct	gat	gac	ctc	att	agc	atg	gga	tcc	aac	gac	att	557
His	Asn	Val	Asp	Ser	Asp	Asp	Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	
		90				95					100					
gag	gta	cta	aag	aaa	att	gac	att	cca	tct	gtc	ttt	att	ggt	gaa	tca	605
Glu	Val	Leu	Lys	Lys	Ile	Asp	Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	
	105				110			115								
tca	gct	agt	tct	ctg	aaa	gat	gaa	ttc	aca	tak	gaa	aaa	ggg	ggc	cac	653
Ser	Ala	Ser	Ser	Leu	Lys	Asp	Glu	Phe	Thr	Xaa	Glu	Lys	Gly	Gly	His	
120				125				130						135		
ctt	atc	tta	ggt	cca	gaa	ttt	agt	ctt	cct	ttg	gaa	tac	tac	cta	att	701
Leu	Ile	Leu	Val	Pro	Glu	Phe	Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	
			140					145						150		
ccc	ttc	ctt	atc	atr	gtg	ggc	atc	tgt	ctc	atc	ttg	ata	gtc	att	ttc	749
Pro	Phe	Leu	Ile	Xaa	Val	Gly	Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	
			155				160						165			
atg	atc	aca	aaa	ttg	tcc	agg	gat	aga	cat	aga	gct	aga	aga	aac	aga	797
Met	Ile	Thr	Lys	Leu	Ser	Arg	Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	
		170				175					180					
ctt	cgt	aaa	gat	caa	ctt	aag	aaa	ctt	cct	gta	cat	aaa	ttc	aag	aaa	845
Leu	Arg	Lys	Asp	Gln	Leu	Lys	Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	
	185				190			195								
gga	gat	gag	tat	gat	gta	tgt	gcc	att	tgt	ttg	gat	gag	tat	gaa	gat	893
Gly	Asp	Glu	Tyr	Asp	Val	Cys	Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	
200				205				210						215		
gga	gac	aaa	ctc	aga	atc	ctt	ccc	tgt	tcc	cat	gct	tat	cat	tgc	aag	941
Gly	Asp	Lys	Leu	Arg	Ile	Leu	Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	
			220				225						230			
tgt	gta	gac	cct	tgg	cta	act	aaa	acc	aaa	aaa	acc	tgt	cca	gtg	tgc	989
Cys	Val	Asp	Pro	Trp	Leu	Thr	Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	
			235				240						245			
agg	caa	aaa	ggt	ggt	cct	tct	caa	ggc	gat	tca	gac	tct	gac	aca	gac	1037
Arg	Gln	Lys	Val	Val	Pro	Ser	Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	
		250				255						260				
agt	agt	caa	gaa	gaa	aat	gaa	gtg	aca	gaa	cat	acc	cct	tta	ctg	aga	1085
Ser	Ser	Gln	Glu	Glu	Asn	Glu	Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	
	265					270					275					
cct	tta	gnc	ttc	tgt	cag	tgc	cca	rgt	cam	ttt	ggg	gct	tta	ntc	gga	1133
Pro	Leu	Xaa	Phe	Cys	Gln	Cys	Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly	

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280          285          290          295
ant ccc gct cac ant cag aak cat gac aga atc att cag act ast gag 1181
Xaa Pro Ala His Xaa Gln Xaa His Asp Arg Ile Ile Gln Thr Xaa Glu
          300          305          310
gaa gac gac aat gaa gat act gac agt agt gat gca gaa gaa 1223
Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp Ala Glu Glu
          315          320          325
tgaaattaat gaacatgatg tcgtggtcca gttgcagcct aatggtgaac gggattacaa 1283
catagcaaact actgtttgac tttcagaaga tgattgggtt atttcccttt aaaatgatta 1343
ggatatatact gtaatttgat tttttgctcc cttaaaagat ttytgtagaa ataacttatt 1403
tttttagtact ytacagttta atcaaattac tgaaacagga cttttgatyt ggtatttatc 1463
tgccaagaat atacttcatt cactaataat agactggtgc tgtaactcaa gcatcaattc 1523
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agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat 117
                                         Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt 165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
-40          -35          -30          -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc 213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
          -20          -15          -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc 261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
          -5          1          5
ttg aag atc att aag gag tat gaa cgt gct gtt gta ttc cgt ctg gga 309
Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg Leu Gly
10          15          20
cgc atc caa gct gac aaa gcc aag ggg cca ggt ttg atc ctg gtc ctg 357
Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu Val Leu
25          30          35          40
cca tgc ata gat gtg ttt gtc aag gtt gac ctc cga aca gtt act tgc 405
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys
          45          50          55
aac att cct cca caa gag atc ctc acc aga gac tcc gta act act cag 453
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln
60          65          70
gta gat gga gtt gtc tat tac aga atc tat agt gct gtc tca gca gtc 501
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val
75          80          85
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gct aat gtc aac gat gtc cat caa gca aca ttt ctg ctg gct caa acc      549
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr
   90                               95                               100
act ctg aga aat gtc tta ggg aca cag acc ttg tcc cag atc tta gct      597
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala
 105                               110                               115                               120
gga cga gaa gag atc gcc cat agc atc cag act tta ctt gat gat gcc      645
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala
                               125                               130                               135
acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg gaa atc aaa gat gtt      693
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val
                               140                               145                               150
cgg att ccc gtg cag ttg cag aga tcc atg gca gcc gag gct gag gcc      741
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala
                               155                               160                               165
acc cgg gaa gcg aga gcc aag gtc ctt gca gct gaa gga gaa atg agt      789
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Ser
                               170                               175                               180
gct tcc aaa tcc ctg aag tca gcc tcc atg gtg ctg gct gag tct ccc      837
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro
 185                               190                               195                               200
ata gct ctc cag ctg cgc tac ctg cag acc ttg agc acg gta gcc acc      885
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr
                               205                               210                               215
gag aag aat tct acg att gtg ttt cct ctg ccc atg aat ata cta gag      933
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu
                               220                               225                               230
ggc att ggt ggc gtc agc tat gat aac cac aag aag ctt cca aat aaa      981
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys
                               235                               240                               245
gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaaaa      1022
Ala

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005760-009E9960

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ctggataagt gctatgtgat ccctctgaac acttccattg ttatgccacc cagaaaccta 180
ctggagttac ttattaacat caaggctgga acctatttgc ctcagtccta tctgattc 238

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atg agc aca tgg tta tta ctg atc gca ttg aaa aca ttg atc acc tgg      286
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
      -25                      -20                      -15
gtt tct tta ttt atc gac tgt gtc atg aca agg aaa ctt aca aac tgc      334
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
      -10                      -5                      1                      5
aac gct aga gaa act att aaa ggt att cag aaa cgt gaa gcc agc aat      382
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
              10                      15                      20
tgt ttc gca att cgg cat ttt gaa aac aaa ttt gcc gtg gaa act tta      430
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
              25                      30                      35
att tgt tct tgaacagcca agaaaaacat tattgaggaa aattaatatc      479
Ile Cys Ser
      40
acagcataac cccacccttt acattttgtg cagtgattat tttttaaaagt cttctttcat      539
gtaagtagca aacagggttt tactatcttt tcatctcatt aattcaatta aaaccattac      599
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005760-00999960

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cgtggcagga aaagtgacta gctccccttc gttgtcagcc agggacgaga acacagccac 120

gctcccaccc ggctgcchaa ggatccctcg gcggcg atg tcg gcc gcc ggt gcc 174

Met Ser Ala Ala Gly Ala

-60

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Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu

-55

-50

-45

atg ctg ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc 270

Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro

-40

-35

-30

aga aca gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt 318

Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys

-25

-20

-15

-10

gct gga ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct 366

Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala

-5

1

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caa tct gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca 414

005760 0093960

Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10 15 20
ctt gta att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt 462
Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe
25 30 35
gtg ggg gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac 510
Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn
40 45 50 55
caa gaa cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc 557
Gln Glu Leu Lys Ala Lys Ala His Lys
60
tgaacaatct agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa 617
agcaaagcta actgtgtgtt tagaaggcac tgtaactggg agctagttct tgattcaata 677
gaaaaatgca gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg 737
gatattagta acatttttct accattttgtc cgtaataaaa catacttgct cgtaaaaaaa 797
aaaaaaa 804

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cagcgggtctt ccagcgttg gccacggcg gcggccctgg gagcagaggt ggagcgaccc 180
cattacgcta aag atg aaa ggc tgg ggt tgg ctg gcc ctg ctt ctg ggg 229
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly
-20 -15 -10
gcc ctg ctg gga acc gcc tgg gct cgg agg agc cgg gat ctc cac tgt 277
Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys
-5 1 5
gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa att gcc cag 325
Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln
10 15 20
gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg atc aat cca 373
Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro
25 30 35 40
gat ggc agc cag tca gtg gtg gag gta act gtt act gkt tcc ccc aaa 421
Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys
45 50 55
aca aaa gta gct cac tct ggc ttt tgg atg aaa att cga ctg ctt aaa 469
Thr Lys Val Ala His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys

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60	65	70	
aaa gga cct tgg tct taatagaaaa tgaagraaaa cagactcaga aaaaaagatt			524
Lys Gly Pro Trp Ser			
75			
tbggctctgt ctcawtttgg aagaaggctg gcaggcttat tccccaatgc aactttgctt			584
cctggctgca aaccyttaat acytttggtt ctgctgtaga aatttgtag ccaaaacawg			644
ggagtcctga twcagcaacc ctttcttcca caatccacca tgactgggtt ttaatgtamc			704
acttggggta tacatgcaaa accatccgtt cmaaaatctg aatycggagc ttaaaaattt			764
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ccaaagtgcg agtccagcgg tcttccagcg cttgggccac ggcggcggcc ctgggagcag 120
aggtggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg 174
Met Lys Gly Trp Gly Trp Leu Ala Leu
-20 -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 222
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10 -5 1 5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa act aga atg gga 270
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Thr Arg Met Gly
10 15 20
aat tgc cca ggt gga ccc caa gaa gac cat tca gat ggg atc ttt ccg 318
Asn Cys Pro Gly Gly Pro Gln Glu Asp His Ser Asp Gly Ile Phe Pro
25 30 35
gat caa tcc aga tgg cag cca gtc agt ggt gga ggt gcc tta tgc ccg 366
Asp Gln Ser Arg Trp Gln Pro Val Ser Gly Gly Gly Ala Leu Cys Pro
40 45 50
ctc aga ggc cca cct cac aga gct gct gga gga gat atg tgaccggatg 415
Leu Arg Gly Pro Pro His Arg Ala Ala Gly Gly Asp Met
55 60 65
aaggagtatg gggaacagat tgatccttcc acccatcgca agaactacgt adgtgtagtg 475
ggccggaatg gagaatccag tgaactggac ctacaaggca tccgaatcga ctgagatatt 535
agcggcaccc tcaagbtttg cgtgtgggaa cattgtggag gaatacgagg atgaactcat 595

005760-009E9950

tgaattcttt	tcccgagagg	ctgacaatgt	taaagacaaa	ctttgcagta	agcgaacaga	655
tctttgtgac	catgccctgc	acatatcggc	atgatgagct	atgaaccact	ggagcagccc	715
acactggcctt	gatggatcac	ccccaggnaa	gggaaaatgg	tggcaatgcc	ttttatatat	775
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<222> 706..711
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005760 00929960

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<221> misc_feature
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ccctgcagtt cgcgwwacag tctctattag agcgcgtgta tagaggcaga kaggagtga      120
gtccacagtt cctctcctcc tagagcctgc cgacc atg ccc gcg ggc gtg ccc      173
                               Met Pro Ala Gly Val Pro
                               -25                               -20

atg tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc      221
Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys
                               -15                               -10                               -5

gca ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata      269
Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
                               1                               5                               10

cct gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga      317
Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
                               15                               20                               25

ctg aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt      365
Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu
30                               35                               40                               45

aaa taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc      418
Lys

ttaatttatt gcatcaaact acttgtcctt aagcacttag tctaattgcta actgcaagag      478
gaggtgctca gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt      538
tcttgaaaac tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg      598
tttagtcttg aatataacgc gaaatagaat atttgtaagt ctactatatg gggtgtcttt      658
atttcatata aattaagaaa ttatttaaaa actatgaact aggtttcatt aaaaaaaaaa      718
gaa                                                                    721

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<222> 235..517
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<222> 52..208
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id :AA524403
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<223> homology
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005760-0096960

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<220>
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<220>
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<221> misc_feature
<222> 227..263
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aggaagttag aaggcccaga ggaggcctcc gggcaaatgg ccggagctgg accgaccatg      120
ctgctacgag aagagaatgg ctgttgcagt cggcgtcaga gcagctccag tgccggggat      180
tcggacggag agcgcgagga ctcggcggct gagcgcgccc gacagcagct agaggcgctg      240
ctcaacaaga ctatgcgcat tcgcatgaca g atg gac gga cac tgg tcg gct      292
                               Met Asp Gly His Trp Ser Ala
                               -40
gct ttc tct gca ctg acc gtg act gca atg tca tcc tgg gct cgg cgc      340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                               -30                               -25                               -20
agg agt tcc tca agc cgt cgg att cct tct ctg ccg ggg agc ccc gtg      388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
                               -15                               -10                               -5
tgc tgg gcc tgg cca tgg tac ccg gac acc aca tcg ttt cca ttg agg      436
Cys Trp Ala Trp Pro Trp Tyr Pro Asp Thr Thr Ser Phe Pro Leu Arg
                               1                               5                               10
tgc aga ggg aga gtc tgaccggggc tccgtatctc tgaccacgat ggcgcttacc      491
Cys Arg Gly Arg Val
15
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<212> DNA
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<223> Von Heijne matrix
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<221> polyA_signal
<222> 736..741
<220>
<221> polyA_site
<222> 770..783
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<221> misc_feature
<222> 207..263
<223> homology
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005760-00929960

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ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgctcct gccaacggtc 180
ggatggcgga gacgaaggac gcagcgcaga tggttggtgac cttcaaggat gtggctgtga 240
cctttacccg ggaggagtgg agacagctgg acctggccca gaggaccctg taccgagagg 300
tgatcgggtt cccaaaccag agttggtcca cctgctagag catgggcagg agctgtggat 360
agtgaagaga ggcctctcac atg cta cct gtg cag agt ttc act ctt gtt gcc 413
Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala
-80 -75
cag gct gga gtg cag tgg cgc cat ctc agc tca ctg caa ctt ctg cct 461
Gln Ala Gly Val Gln Trp Arg His Leu Ser Ser Leu Gln Leu Leu Pro
-70 -65 -60
ccc gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat 509
Pro Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp
-55 -50 -45
tac agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta 557
Tyr Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val
-40 -35 -30 -25
gag acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc 605
Glu Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr
-20 -15 -10
tca tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc 653
Ser Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly
-5 1 5
gtg agc cac gtg ccc ggc aaa aaa aaa ctg ctt aag gtt gaa aag aaa 701
Val Ser His Val Pro Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys
10 15 20
aat tta aga aaw ttg ctg acg gra ata aaa acy taataaaaact accacccgaa 754
Asn Leu Arg Xaa Leu Leu Thr Xaa Ile Lys Thr
25 30 35
ggaatgaaaa aaccaaaaaa aaaaaaaaaa 783

<210> 68
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<213> Homo sapiens
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<222> 140..205
<223> Von Heijne matrix
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<221> misc_feature
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<222> 609..679

00563500-094500

<223> homology
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<223> homology

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est

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<223> homology

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<400> 68

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ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg 120

gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc 172

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile

-20

-15

ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc 220

Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg

-10

-5

1

5

aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt 268

Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe

10

15

20

gak ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag 316

Xaa Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys

25

30

35

gta tgt ggt cgt ggc ava cgg ggt ctc cag agg aga caa tgc ttt ctt 364

Val Cys Gly Arg Gly Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu

40

45

50

ttt taaactttct ttcattgact cttaagtgcg gggctagaac acggggaaca 417

Phe

tacctgcttg cctcaaacta aaggatctag tcmtytctga aktcctctac tsacrtrtra 477

caacaatatc ctgtgcaaaa ttttgcgaaa gaaatgaaat acaattgcmg cgtgcatcga 537

cattttttgga agtagagatt aacyyttcgt atttttactt cmtcgaagtt aagttccaaa 597

tgtgtatgtg ttaagtaaat gttttcagta aytgggaaag ataaagtgtg atccaattta 657

agtttgtgaa aatgagtaat tccgtatcca aaytggagtt aacaccaaag tattgtacaa 717

attgcttgca cagttgggtcc gtacacaata gacaggctyt gtatttttag ctgacgttgt 777

tatttgatga tgatgtactc cattttcamt acggcccgaag gagamtagta atcctccttg 837

tagtagatgt ttttgtcttg aaagtatctt ttaaattgtyt gagcacttta aggaacagac 897

ccttattaat gtyttttaag ttttattcaa tttccagtca caaatatttt atggtatttg 957

attgtytaat aaatttgtat gatattaaaa aaaaaaaaaa 996

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<223> Von Heijne matrix

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005760-00959560

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agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac      120
ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgctct gccaacggtc      180
gg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      227
  Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
      -50              -45              -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
      -35              -30              -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
      -20              -15              -10
ctg gtt tca cta ggg caa agc att tgg ctg cat ata aca gaa aac cag      371
Leu Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln
      -5              1              5              10
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      419
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
      15              20              25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag      467
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
      30              35              40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctggatt      527
gtcctcaggc tggctcctca tagggatgct ggggtgctgca gccttgactg gggcagcagg      587
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aaaaaaaaaa      657

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<222> 225..316
<223> homology
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gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc 172
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
-20 -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc 220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
-10 -5 1 5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt 268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
10 15 20
gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag 316
Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
25 30 35
tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg acc ttt 364
Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe
40 45 50
gtt act gaa gaa gga agg aat taatgtgttt ctaaaatcca aaaaaaaaaa a 416
Val Thr Glu Glu Gly Arg Asn
55 60

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<223> n=a, g, c or t
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actgtcccat tcctccccct acaacacaca cacctttcag gcagggasgn gatgagcttc 60
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gtgtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca tgt agc 170
 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser
 -15 -10 -5
aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt ctc ccc 218
Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro
 1 5 10
agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc tgc agg 266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
15 20 25 30
cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc ctc cac 314
Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His
 35 40 45
ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc tgg gac 362
Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp
 50 55 60
tgg gct gag gca ggg gct tgg ctc tat tct ccc taaccatact gtcttccttt 415
Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 65 70
cccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct cccttgcctt 475
ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa gtgaaaaaaa 535
aaaaaaaaa 543

<210> 72
<211> 605
<212> DNA
<213> Homo sapiens
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<222> 592..605
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<222> 348..432
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cttccgaaaa gagacagaca atgcagccat cataatgaag gtggacaaag accggcagat 180

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ggtggtgctg gaggaagaat ttcagaacat ttccccagag gagctcaaaa tggagttgcc 240
ggagagacag cccaggttcg tggtttacag ctacaagtac gtgc atg acg atg gcc 296
Met Thr Met Ala
gag tgt cct acc ctt tgt gtt tca tct tct cca gcc ctg tgg gct gca 344
Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala Leu Trp Ala Ala
-15 -10 -5 1
agc gaa aca aca gat gat gta tgc agg gag taaaaacagg ctggtgcaga 394
Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
5 10
cagcagagct caciaagggtg ttcgaaatcc gcaccactga tgacctcact gaggcctggc 454
tccaagaaaa gttgtctttc tttcgttgat ctctgggctg gggactgaat tcctgatgct 514
tgagtcctca aggtgactgg ggacttggaa cccctaggac ctgaacaacc aaggacttta 574
aataaatttt aaaatgcaaa aaaaaaaaaa a 605

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<222> 587..668
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cgctgttccc caggr atg gtg atc cgt gta tat att gca tct tcc tct ggc 171
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
-100 -95
tct aca gcg att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa 219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-90 -85 -80
gcc aac aaa ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag 267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-75 -70 -65 -60
aat cgg aag tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc 315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
-55 -50 -45
aca ggt aac ccc ctg cca cct cag att ttc aat gaa agc cag tat cgc 363
Thr Gly Asn Pro Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg
-40 -35 -30
ggg gac tat gat gcc ttc ttt gaa gcc aga gaa aat aat gca gtg tat 411
Gly Asp Tyr Asp Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr
-25 -20 -15
gcc ttc tta ggc ttg aca gcc cca tct ggt tca aag gaa gca gga agg 459
Ala Phe Leu Gly Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg
-10 -5 1 5

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tgc aag caa agc agc aag cca tgaaccttga gcactgtgct ttttaagcatc 510
Cys Lys Gln Ser Ser Lys Pro

10

ctgaaaaatg agtctccatt gctttttataa aatagcagaa ttagcttttgc sttcaaaaga 570
aataggstta atgttgaaat aatagattag ttgggttttc acatgcaaac amtcaaaatg 630
aatacaaaat taaaatttga acattatggt gattatggtg aggagaatgg gatattaaca 690
taaaattata ttaataagta gatatygtag aaatagtgtt gttacctgcc aagccatcct 750
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005760-0099960

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cctgaagtga cagcggagag aaccaggcag cccagaaacc ccaggcgtgg agattgatcc 120
tgcgagagaa ggggggttcat catggcggat gacctaaagc gattcttgta taaaaagtta 180
ccaagtgttg aagggctcc atg cca ttg ttg tgt cag ata gag atg gag tac 232
 Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
 -75 -70
ctg tta tta aag tgg caa atg aca atg ctc cag agc atg ctt tgc gac 280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65 -60 -55 -50
ctg gtt tct tat cca ctt ttg ccc ttg caa cag acc aag gaa gca aac 328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
 -45 -40 -35
ttg gac ttt cca aaa ata aaa gta tca tct gtt act ata aca cct acc 376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
 -30 -25 -20
agg tgg ttc aat tta atc gtt tac ctt tgg gtg gtg agt ttc ata gcc 424
Arg Trp Phe Asn Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
 -15 -10 -5
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt 472
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
 1 5 10 15
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct 514
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
 20 25
taatctgaca gtgggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc 574
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccttttttc 634
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt 694

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09663600-091500

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<222> 517..595
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ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac	120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag	180
tctgaagagc agccagtgtt tcggcttggtg ccctgtatac ttgaagctgc caaacaagta	240
cgttctgaaa atccagaatg gcttgatggt tac atg cac att tta caa ctg ctt	294
Met His Ile Leu Gln Leu Leu	
-40	

act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act	342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr	
-35 -30 -25 -20	

gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc	390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe	
-15 -10 -5	

tgc cag tct gat gat cca gcc atc att ctt caa gaa cag aaa aca gtg	438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Glu Gln Lys Thr Val	
1 5 10	

cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act	486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr	
15 20 25	

gag caa gag tat cta aag ata gaa aaa gta gat ctt cct cta att gac	534
Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu Pro Leu Ile Asp	
30 35 40 45	

agc ctc att cgg gtc tta caa aat atg gaa cag tgt cag aaa aaa cca	582
Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys Gln Lys Lys Pro	
50 55 60	

gag aac tcg gca gga gtc taacacagag gaaactaaaa ggactgattt	630
Glu Asn Ser Ala Gly Val	
65	

aaccaagat gatttccact tgaaaatctt aaaaggatat tgttatgggtg aagtttctgt	690
ctaataattht ttcaggcatt aacaaaggag acggtggctc agggagtaaa ggaaggccgt	750
tgagcaaaca gaagtgttcc tctgcaattht caaaarcctt cttcttttcta tagcccctgt	810
gggtggaaga ttttattaaa atcctacgtg aagttgataa ggcgcttgct kgatgacttg	870
gaaaaaaamc ttcccaagtt tgaaggttca gaastaaaaa rscktgaatg ggaattactt	930
sstgtbcaag aaaataaact ttatttttct cactgaaaaa aaaaaaaa	978

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096300-091500

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gaaaccagaa gaaaaatatg agacggggaa tcatcgtgtg atgtgtgtgc tgcctttggc      120
tkwgtgtgk gaagtycckg ctcaggtgtt aggtacagtg tgtttgatcg tgggtggcttg      180
aggggaaccc gctgttcaga gctgtgactg cggctgcact cagagaagct gcccttggct      240
gctcgtagcg ccgggccttc tctcctcgtc atcatccaga gcagccagtg tccgggaggg      300
agaagatgcc ccactccagc ctctggactg ggggctctct tcagtggctg aatgtccagc      360
agagctattt ccttccacag ggggccttgc aggggaagggt ccaggacttg acatcttaag      420
atg cgt ctt gtc ccc ttg ggc cag tca ttt ccc ctc tct gag cct cgg      468
Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
-15 -10 -5 1
tgt ctt caa cct gtg aaa tgg gat cat aat cac tgc ctt acc tcc ctc      516
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
5 10 15
acg gtt gtt gtg agg act gag tgt gtg gaa gtt ttt cat aaa ctt tgg      564
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
20 25 30
atg cta gtg taaaaaaaaa aaaa      587
Met Leu Val
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tctgactcca tggaaaccag atgggggcaac ggggtggttc tagtgcagac tgtagctgca      120
gctcctctcc acctctagcc tgctcatttc cagctcagaa attctactaa tggcgttttt      180
tcttcttgaa aaaggaa atg aac agg gtc cct gct gat tct cca aat atg      230
      Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
      -25 -20
tgt cta atc tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca      278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
-15 -10 -5
aaa atc tgt aga aga gca ttc cag gaa gag gga aga gca aat gca aag      326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys
1 5 10 15
acg ggc gtg aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc      375
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Thr Gly Val Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
 20 25

ttggaatagc caaaaaaaaa aaaaa

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ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga cagccaggag cggttttctg      120
ggaactgtgg gatgtgccct tggggggcccg agaaaacaga aggaag atg ctc cag      175
                                   Met Leu Gln
                                   -20
acc agt aac tac agc ctg gtg ctc tct ctg cag ttc ctg ctg ctg tcc      223
Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu Leu Leu Ser
      -15                                -10                                -5
tat gac ctc ttt gtc aat tcc ttc tca gaa ctg ctc caa aag act cct      271
Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro
      1                                5                                10
gtc atc cag ctt gtg ctc ttc atc atc cag gat att gca gtc ctc ttc      319
Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala Val Leu Phe
15                                20                                25                                30
aac atc atc atc att ttc ctc atg ttc ttc aac acc tcc gtc ttc cag      367
Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser Val Phe Gln
      35                                40                                45
gct ggc ctg gtc aac ctc cta ttc cat aag ttc aaa ggg acc atc atc      415
Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly Thr Ile Ile
      50                                55                                60
ctg aca gct gtg tac ttt gcc ctc agc atc tcc ctt cat gtc tgg gtc      463
Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His Val Trp Val
      65                                70                                75
atg aac tta cgc tgg aaa aac tcc aac agc ttc ata tgg aca gat gga      511
Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp Thr Asp Gly
      80                                85                                90
ctt caa atg ctg ttt gta ttc cag aga cta gca gca gtg ttg tac tgc      559
Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val Leu Tyr Cys
95                                100                                105                                110

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tac ttc tat aaa cgg aca gcc gta aga cta ggc gat cct cac ttc tac	607
Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro His Phe Tyr	
115 120 125	
cag gac tct ttg tgg ctg cgc aag gag ttc atg caa gtt cga agg	652
Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val Arg Arg	
130 135 140	
tgacctcttg tcacactgat ggatactttt ccttcctgat agaagccaca tttgctgctt	712
tgcagggaga gttggcccta tgcattggga aacagctgga ctttccaagg aagggttcaga	772
ctagctgtgt tcagcattca agaaggaaga tccccctct tgcacaatta gagtgcctcc	832
atcggctctcc agtgcggcat cccttccttg ccttctacct ctgttccacc cccttccttc	892
ctctcctctc tgtaccattc attctccctg accggccttt cttgccgagg gttctgtggc	952
tcttaccctt gtgaagcttt tccttttagcc tgggacagaa ggacctcccg gcccccaaag	1012
gatctcccag wtgaccaaag gatgcgaaga gtgatagtta cgntgctcct gactgatcac	1072
accgcagaca tttagatttt tatacccaag gcacttttaa aaaatgtttt ataaatagag	1132
aataaattga attyttgttc caaaaaaaaaaaaa	1166

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ggcctgctgg	gcttggcaac	gagggactcg	gcctcggagg	cgacccagac	cacacagaca	120
ctgggtcaag	gagtaagcag	aggataaaca	actggaagga	gagcaagcac	aaagtcac	179
atg gct tca	gcg tct gct	cgt gga aac	caa gat aaa	gat gcc cat	ttt	227
Met Ala Ser	Ala Ser Ala	Arg Gly Asn	Gln Asp Lys	Asp Ala His	Phe	
	-65		-60		-55	
cca cca cca	agc aag cag	agc ctg ttg	ttt tgt cca	aaa tca aaa	ctg	275
Pro Pro Pro	Ser Lys Gln	Ser Leu Leu	Phe Cys Pro	Lys Ser Lys	Leu	
	-50		-45		-40	
cac atc cac	aga gca gag	atc tca aag	att atg cga	gaa tgt cag	gaa	323
His Ile His	Arg Ala Glu	Ile Ser Lys	Ile Met Arg	Glu Cys Gln	Glu	
	-35		-30		-25	
gaa agt ttc	tgg aag aga	gct ctg cct	ttt tct ctt	gta agc atg	ctt	371
Glu Ser Phe	Trp Lys Arg	Ala Leu Pro	Phe Ser Leu	Val Ser Met	Leu	
	-20		-15		-10	
					-5	
gtc acc cag	gga cta gtc	tac caa ggt	tat ttg gca	gct aat tct	aga	419
Val Thr Gln	Gly Leu Val	Tyr Gln Gly	Tyr Leu Ala	Ala Ala Asn	Ser Arg	

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ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc			467
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly			
15	20	25	
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt			515
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe			
30	35	40	
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt ccw aca gca			557
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala			
45	50	55	
taacaggcac tgcctcctta cctgtgagga atgcaaaata aagcatggat taagtgagaa			617
gggagactct cagccttcag cttcctaaat tctgtgtctg tgactttcga agttttttaa			677
acctctgaat ttgtacacat ttaaaatttc aaggtgtact ttaaaatnaa aatacttcta			737
atgtvaaaaa aaaaaaa			754

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 atg acc agc atg act cag tct ctg cgg gag gtg ata aag gcc atg acc 226
 Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
 -40 -35 -30 -25
 aag gct cgc aat ttt gag aga gtt ttg gga aag att act ctt gtc tct 274
 Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
 -20 -15 -10
 gct gct cct ggg aaa gtg att tgt gaa atg aaa gta gaa gaa gag cat 322
 Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
 -5 1 5
 acc aat gca ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta 370
 Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
 10 15 20
 gat aac ata tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc 418
 Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
 25 30 35 40
 gga gtc agt gtc gat atg aac ata acg tac atg tca cct gca aaa tta 466
 Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
 45 50 55
 gga gag gat ata gtg att aca gca cat gtt ctg aag caa gga aaa aca 514

005160-009990

Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His	Val	Leu	Lys	Gln	Gly	Lys	Thr		
			60					65				70					
ctt	gca	ttt	acc	tct	gtg	ggt	ctg	acc	aac	aag	gcc	aca	gga	aaa	tta		562
Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys	Leu		
		75					80				85						
ata	gca	caa	gga	aga	cac	aca	aaa	cac	ctg	gga	aac	tgagagaaca					608
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn						
	90					95				100							
gcagaatgac	ctaaagaaac	ccaacaatga	atatcaagta	tagatttgac	tcaaacaatt												668
gtaatttttg	aaataaacta	gcaaaaccaa	aaaaaaaaaa	g													709

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<210> 82
<211> 243
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
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<223> Von Heijne matrix
      score 3.70000004768372
      seq ILFNLLIFLCGFT/NY
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<221> polyA_signal
<222> 211..216
<220>
<221> polyA_site
<222> 230..243
<220>
<221> misc_feature
<222> 2..164
<223> homology
      id :H64488
      est
<220>
<221> misc_feature
<222> 2..164
<223> homology
      id :AA131065
      est
<220>
<221> misc_feature
<222> 5..164
<223> homology
      id :AA224847
      est
<220>
<221> misc_feature
<222> 10..164
<223> homology
      id :AA161042
      est
<220>
<221> misc_feature
<222> 2..84
<223> homology
      id :AA088770
      est
<220>

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005760-003E9960

<221> misc_feature
<222> 104..164
<223> homology
 id :AA088770
 est
<220>
<221> misc_feature
<222> 10..164
<223> homology
 id :AA100852
 est
<220>
<221> misc_feature
<222> 79..164
<223> homology
 id :AA146774
 est
<220>
<221> misc_feature
<222> 79..164
<223> homology
 id :AA146605
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<220>
<221> misc_feature
<222> 109..164
<223> homology
 id :AA299239
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<220>
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<222> 158..207
<223> homology
 id :AA037885
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<220>
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<222> 160..207
<223> homology
 id :AA480512
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<222> 160..207
<223> homology
 id :AA468030
 est
<220>
<221> misc_feature
<222> 160..207
<223> homology
 id :AA420727
 est
<220>
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<222> 160..207
<223> homology
 id :AA574382

005750 0099960

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      est
<220>
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<222> 160..207
<223> homology
      id :AA133048
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<220>
<221> misc_feature
<222> 200..229
<223> homology
      id :AA469266
      est
<220>
<221> misc_feature
<222> 200..229
<223> homology
      id :AA550735
      est
<220>
<221> misc_feature
<222> 200..229
<223> homology
      id :AA601071
      est
<220>
<221> misc_feature
<222> 200..229
<223> homology
      id :AA225190
      est
<400> 82
aactcagtgg caacacccgg gagctgtttt gtcctttgtg gagcctcagc agttccctct      60
ttcagaactc actgccaaga gccctgaaca ggagccacc atg cag tgc ttc agc      114
                                   Met Gln Cys Phe Ser
                                   -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt      162
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
                                   -15      -10      -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg      210
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
                                   1      5      10
cat aaa cct gtt aca atg taaaaaaaa aaaaa      243
His Lys Pro Val Thr Met
      15

<210> 83
<211> 829
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 346..408
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTS/AF
<220>
<221> polyA_signal
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005760.0093960

<222> 792..797
<220>
<221> polyA_site
<222> 817..829
<220>
<221> misc_feature
<222> 260..464
<223> homology
 id :H57434
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<220>
<221> misc_feature
<222> 118..184
<223> homology
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 est
<220>
<221> misc_feature
<222> 56..113
<223> homology
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 est
<220>
<221> misc_feature
<222> 454..485
<223> homology
 id :H57434
 est
<220>
<221> misc_feature
<222> 118..545
<223> homology
 id :N27248
 est
<220>
<221> misc_feature
<222> 65..369
<223> homology
 id :H94779
 est
<220>
<221> misc_feature
<222> 471..519
<223> homology
 id :H94779
 est
<220>
<221> misc_feature
<222> 61..399
<223> homology
 id :H09880
 est
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<222> 408..452
<223> homology
 id :H09880
 est

005150-0094960

<220>
<221> misc_feature
<222> 60..399
<223> homology
 id :H29351
 est

<220>
<221> misc_feature
<222> 393..432
<223> homology
 id :H29351
 est

<220>
<221> misc_feature
<222> 260..444
<223> homology
 id :AA459511
 est

<220>
<221> misc_feature
<222> 449..545
<223> homology
 id :AA459511
 est

<220>
<221> misc_feature
<222> 117..184
<223> homology
 id :AA459511
 est

<220>
<221> misc_feature
<222> 122..399
<223> homology
 id :T74091
 est

<220>
<221> misc_feature
<222> 393..434
<223> homology
 id :T74091
 est

<220>
<221> misc_feature
<222> 61..378
<223> homology
 id :HSC3CB081
 est

<220>
<221> misc_feature
<222> 118..399
<223> homology
 id :T82010
 est

<220>
<221> misc_feature
<222> 268..545
<223> homology

009563600.097500

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id :W02860
est
<220>
<221> misc_feature
<222> 268..545
<223> homology
      id :N44490
      est
<220>
<221> misc_feature
<222> 115
<223> n=a, g, c or t
<400> 83
actccttttta gcataggggc ttcggcgcca gcggccagcg ctagtcggtc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttcctg agaaaatcag cggctctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctggt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                   Met Trp Trp Phe
                                   -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                               -10                               -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                               5                               10                               15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
      20                               25                               30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                               40                               45
aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa      602
Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt      662
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact tggataaata      722
tggttaaggtg ggcttttccc cctgtgtaat tggctacsac gtcttacttg agccaagttg      782
gtaagttgaa ataaatgat watgagagtg acacavaaaa aaaaaaa      829

<210> 84
<211> 674
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 177..233
<223> Von Heijne matrix
      score 6.09999990463257
      seq LALLWSLPASDLG/RS
<220>
<221> polyA_signal
<222> 644..649
<220>
<221> polyA_site
<222> 663..674
<220>
<221> misc_feature

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09663600-091500

<222> 194..592
<223> homology
 id :AA496246
 est
<220>
<221> misc_feature
<222> 1..100
<223> homology
 id :AA496246
 est
<220>
<221> misc_feature
<222> 99..202
<223> homology
 id :AA496246
 est
<220>
<221> misc_feature
<222> 187..592
<223> homology
 id :AA476481
 est
<220>
<221> misc_feature
<222> 594..661
<223> homology
 id :AA476481
 est
<220>
<221> misc_feature
<222> 188..592
<223> homology
 id :AA496245
 est
<220>
<221> misc_feature
<222> 594..661
<223> homology
 id :AA496245
 est
<220>
<221> misc_feature
<222> 194..444
<223> homology
 id :AA476480
 est
<220>
<221> misc_feature
<222> 1..102
<223> homology
 id :AA476480
 est
<220>
<221> misc_feature
<222> 99..187
<223> homology
 id :AA476480
 est

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<220>
<221> misc_feature
<222> 437..592
<223> homology
      id :AA505488
      est
```

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<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA505488
      est
```

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<220>
<221> misc_feature
<222> 441..592
<223> homology
      id :AA554685
      est
```

```
<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA554685
      est
```

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<220>
<221> misc_feature
<222> 414..503
<223> homology
      id :AA215595
      est
```

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<220>
<221> misc_feature
<222> 510..539
<223> homology
      id :AA215595
      est
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<400> 84																		
ataagtgaac			cagaccaccc			tgatggcatc			cacagtgatg			tcaagggttgg			ggctggccag			60
gggtgggtgg			actagaagca			tttgggagta			gtggccaggg			gccctggacg			ctagccacgg			120
agctgctgca			cagagcctgg			tgtccacaag			cttccaggtt			ggggttggag			cctggg atg			179
															Met			
agc ccc ggc			agc gcc ttg			gcc ctt ctg			tgg tcc ctg			cca gcc tct			gac			227
Ser Pro Gly			Ser Ala Leu			Ala Leu Leu			Trp Ser Leu			Pro Ala Ser			Asp			
			-15						-10						-5			
ctg ggc cgg			tca gtc att			gct gga ctc			tgg cca cac			act ggc gtt			ctc			275
Leu Gly Arg			Ser Val Ile			Ala Gly Leu			Trp Pro His			Thr Gly Val			Leu			
			1			5						10						
atc cac ttg			gaa aca agc			cag tct ttt			ctg caa ggt			cag ttg acc			aag			323
Ile His Leu			Glu Thr Ser			Gln Ser Phe			Leu Gln Gly			Gln Leu Thr			Lys			
15			20						25						30			
agc ata ttt			ccc ctc tgt			tgt aca tcg			ttg ttt tgt			gtt tgt gtt			gta			371
Ser Ile Phe			Pro Leu Cys			Cys Thr Ser			Leu Phe Cys			Val Cys Val			Val			
			35			40						45						
aca gtg ggt			gga ggg agg			gtg ggg tct			aca ttt gtt			gca tgagtcgatg						420
Thr Val Gly			Gly Gly Arg			Val Gly Ser			Thr Phe Val			Ala						
			50			55												
ggtcagaact			ttagtatacg			catgcgtcct			ctgagtgaca			gggcatttttg			tcgaaaataa			480
gcaccttggt			aactaaaccc			ctctaatagc			tataaaggct			ttagttctgt			attgattaag			540

ttactgtaaa agcttggggtt tatttttgta ggacttaatg gctaagaatt agggaacata	600
gcaagggggc tcctctgttg gagtaatgta aattgtaatt ataaataaac atgcaaacct	660
ttaaaaaaaaaaaaa	674

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<210> 85
<211> 478
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 179..319
<223> Von Heijne matrix
      score 5.5
      seq SALLFFARPCVFC/FK
<220>
<221> polyA_signal
<222> 461..466
<220>
<221> polyA_site
<222> 465..478
<220>
<221> misc_feature
<222> 2..464
<223> homology
      id :AA310996
      est
<220>
<221> misc_feature
<222> 8..464
<223> homology
      id :AA312901
      est
<220>
<221> misc_feature
<222> 2..416
<223> homology
      id :AA401411
      est
<220>
<221> misc_feature
<222> 2..349
<223> homology
      id :R64030
      est
<220>
<221> misc_feature
<222> 56..464
<223> homology
      id :AA400108
      est
<220>
<221> misc_feature
<222> 126..273
<223> homology
      id :AA010825
      est
<220>
<221> misc_feature

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005150.005150.005150

005160.009990

<222> 2..147
<223> homology
 id :AA010825
 est
<220>
<221> misc_feature
<222> 358..435
<223> homology
 id :AA010825
 est
<220>
<221> misc_feature
<222> 78..464
<223> homology
 id :AA504732
 est
<220>
<221> misc_feature
<222> 90..441
<223> homology
 id :H60506
 est
<220>
<221> misc_feature
<222> 59..349
<223> homology
 id :AA346780
 est
<220>
<221> misc_feature
<222> 2..331
<223> homology
 id :AA281167
 est
<220>
<221> misc_feature
<222> 6..236
<223> homology
 id :R35805
 est
<220>
<221> misc_feature
<222> 232..284
<223> homology
 id :R35805
 est
<220>
<221> misc_feature
<222> 41..307
<223> homology
 id :H13784
 est
<220>
<221> misc_feature
<222> 2..40
<223> homology
 id :H13784
 est

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<220>
<221> misc_feature
<222> 64..280
<223> homology
      id :AA128122
      est

<220>
<221> misc_feature
<222> 293..349
<223> homology
      id :AA128122
      est

<220>
<221> misc_feature
<222> 332..385
<223> homology
      id :AA128122
      est

<220>
<221> misc_feature
<222> 163..420
<223> homology
      id :AA555127
      est

<400> 85
aagtccttcg cgccctcctc gccctcccca ccgacatcat gctccagttc ctgcttggat      60
ttacactggg caacgtgggt ggaatgtatc tggctcagaa ctatgatata ccaaacctgg      120
ctaaaaaact tgaagaaatt aaaaaggact tggatgccaa gaagaaaccc cctagtgc      178
atg aga ctg cct cca gca ctg cct tca gga tat act gat tct act gct      226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
      -45                      -40                      -35

ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt tcg tct      274
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
      -30                      -25                      -20

cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt tgc ttt      322
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
      -15                      -10                      -5                      1

aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca ttt cca      370
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
      5                      10                      15

aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg agg ttc      418
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
      20                      25                      30

taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa aaaaacaaaa      478

<210> 86
<211> 952
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 112..237
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIT/FP

<220>
<221> polyA_signal
<222> 910..915

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005150 0093990 0963900 091500

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<220>
<221> polyA_site
<222> 940..952
<400> 86
aatacttttct cctctcccct ctcccaagca catctgagtt gctgcctggt cttcacactt      60
agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat      117
                                     Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
-40                               -35                               -30                               -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
                               -20                               -15                               -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
                               -5                               1                               5
ttg aag att tgatcctggt cctgccatgc ataratgtgt ttgtcaaagt      310
Leu Lys Ile
10
tgacctccga acagttactt gcaacattcc tccacaagag atcctcacca rgagactccg      370
taactactca ggtagatgga gttgtctatt acagaatcta tagtgctgtc tcagcagtgg      430
ctaakgtcaa cgatgtccat caagcaacat ttctgctggc tcaaaccact ctgagaaatg      490
tcktagggac acaggacctt gtccccagat cttaggctgg acgagaagag atcgcccata      550
agcatccaga ctktacttga tgatgccacc gaactggtgg gggatccggg tggcccagat      610
ggaaatcaaa gatgttcgga ttcccgtgca gttgcagaga tccatggcag ccgaggstga      670
ggccaccgga gaagsgagag ccaaggtcct tgcagctgaa ggagaaatga atgsttccaa      730
atccctgaag tcagcctcca tgggtgstggs tgagtytccc atagctytcc agstgsgsta      790
cctgcagacc ttgagcacgg tagccaccga gaagaatttt acgattgtgt ttcctbtgcc      850
catgaatata ctagagggca ttggtggcgt cagstatgat aaccacaaga agsttbscaa      910
ataaagcctg aggtcybctt gcggtagtca aaaaaaaaaa aa      952

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<210> 87
<211> 131
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -13..-1
<400> 87
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
                               -10                               -5                               1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5                               10                               15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20                               25                               30                               35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
                               40                               45                               50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
55                               60                               65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
70                               75                               80
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
85                               90                               95
Gly Arg Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp
100                               105                               110                               115
Tyr Leu Lys

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<210> 88

<211> 63
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -35...-1
 <400> 88
 Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
 -35 -30 -25 -20
 His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
 -15 -10 -5
 Val Phe Ser Leu Lys Gln Leu Lys Lys Lys Ser Trp Ser Lys Tyr Leu
 1 5 10
 Phe Glu Ser Cys Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile
 15 20 25

<210> 89
 <211> 163
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -31...-1
 <220>
 <221> UNSURE
 <222> 91,108,109,112,124
 <223> Xaa = any one of the twenty amino acids
 <400> 89
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -30 -25 -20
 Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys
 -15 -10 -5 1
 Ser Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn
 5 10 15
 Ile Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro
 20 25 30
 Ser Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys
 35 40 45
 Pro Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp
 50 55 60 65
 Pro Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr
 70 75 80
 Ser Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg
 85 90 95
 Gly Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys
 100 105 110
 Gly Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr
 115 120 125
 Pro Pro Pro
 130

<210> 90
 <211> 52
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1

0051500.0099990

005760-00999999

<400> 90

Met	Leu	Gly	Thr	Thr	Gly	Leu	Gly	Thr	Gln	Gly	Pro	Ser	Gln	Gln	Ala
		-30					-25					-20			
Leu	Gly	Phe	Phe	Ser	Phe	Met	Leu	Leu	Gly	Met	Gly	Gly	Cys	Leu	Pro
	-15					-10					-5				
Gly	Phe	Leu	Leu	Gln	Pro	Pro	Asn	Arg	Ser	Pro	Thr	Leu	Pro	Ala	Ser
1				5					10					15	
Thr	Phe	Ala	His												
			20												

<210> 91

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -97...-1

<400> 91

Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe	Leu	Tyr	Lys	Lys	Leu	Pro	Ser	Val
		-95					-90					-85			
Glu	Gly	Leu	His	Ala	Ile	Val	Val	Ser	Asp	Arg	Asp	Gly	Val	Pro	Val
	-80					-75					-70				
Ile	Lys	Val	Ala	Asn	Asp	Asn	Ala	Pro	Glu	His	Ala	Leu	Arg	Pro	Gly
-65					-60					-55					-50
Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly
				-45					-40					-35	
Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val
			-30					-25					-20		
Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser
	-15					-10						-5			
Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro
1					5					10					15
Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Ile	Ser				
				20					25						

<210> 92

<211> 230

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<220>

<221> UNSURE

<222> 54,79

<223> Xaa = any one of the twenty amino acids

<400> 92

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Leu
			-20						-15					-10	
Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	Lys	Thr
		-5						1				5			
Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	Phe	Ser	Lys
10					15						20				
Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	Ile	Thr	Gln	Cys
25					30					35					40
Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	Asp	Ile	Xaa	Ala	Ala
				45					50					55	
Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile

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			60					65				70					
Ile	Ser	Val	Val	Gly	Met	Xaa	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg		
		75					80					85					
Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly		
	90					95					100						
Gly	Leu	Leu	Gly	Phe	Ile	Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu		
105					110					115					120		
Arg	Asp	Phe	Tyr	Ser	Pro	Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile		
				125					130					135			
Gly	Glu	Ala	Leu	Tyr	Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile		
			140					145					150				
Ala	Gly	Ile	Ile	Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser		
		155					160					165					
Asn	Tyr	Tyr	Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser		
170						175					180						
Pro	Arg	Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr		
185					190					195					200		
Ser	Leu	Thr	Gly	Tyr	Val												
				205													

<210> 93
 <211> 72
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1
 <400> 93

Met	Phe	Ala	Pro	Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu		
		-30					-25					-20					
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Val	Gly	Gly	Ser	Phe	Gly		
	-15					-10					-5						
Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Ser	Lys	Met		
1				5				10						15			
Asp	Pro	Glu	Leu	Glu	Lys	Lys	Pro	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu		
			20					25					30				
Ser	Glu	Tyr	Glu	Gly	Ser	Ile	Cys										
		35					40										

<210> 94
 <211> 91
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -36...-1
 <400> 94

Met	Asn	Thr	Phe	Glu	Pro	Asp	Ser	Leu	Ala	Val	Ile	Ala	Phe	Phe	Leu		
	-35					-30					-25						
Pro	Ile	Trp	Thr	Phe	Ser	Ala	Leu	Thr	Phe	Leu	Phe	Leu	His	Leu	Pro		
-20					-15					-10					-5		
Pro	Ser	Thr	Ser	Leu	Phe	Ile	Asn	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Gly		
				1				5					10				
Pro	Leu	Gly	Leu	Ile	Leu	Leu	Leu	Ser	Phe	Cys	Gly	Gly	Tyr	Thr	Lys		
		15				20						25					
Cys	Asp	Phe	Ala	Leu	Ser	Tyr	Leu	Glu	Ile	Pro	Asn	Arg	Ile	Glu	Phe		
30						35					40						
Ser	Ile	Met	Asp	Pro	Lys	Arg	Lys	Thr	Lys	Cys							

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 97

Met	Cys	Phe	Pro	Glu	His	Arg	Arg	Gln	Met	Tyr	Ile	Gln	Asp	Arg	Leu
		-40					-35					-30			
Asp	Ser	Val	Thr	Arg	Arg	Ala	Arg	Gln	Gly	Arg	Ile	Cys	Ala	Ile	Leu
	-25					-20				-15					
Leu	Leu	Gln	Ser	Gln	Cys	Ala	Tyr	Trp	Ala	Leu	Pro	Glu	Pro	Arg	Thr
-10					-5					1				5	
Leu	Asp	Gly	Gly	His	Leu	Met	Gln								
					10										

<210> 98

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22...-1

<400> 98

Met	Gln	Asn	His	Leu	Gln	Thr	Arg	Pro	Leu	Phe	Leu	Thr	Cys	Leu	Phe
		-20					-15					-10			
Trp	Pro	Leu	Ala	Ala	Leu	Asn	Val	Asn	Ser	Thr	Phe	Glu	Cys	Leu	Ile
	-5				1				5						10
Leu	Gln	Cys	Ser	Val	Phe	Ser	Phe	Ala	Phe	Phe	Ala	Leu	Trp		
				15				20							

<210> 99

<211> 251

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<220>

<221> UNSURE

<222> 54,131,132,140,179,194,213,221

<223> Xaa = any one of the twenty amino acids

<400> 99

Met	Trp	Arg	Leu	Leu	Ala	Arg	Ala	Ser	Ala	Pro	Leu	Leu	Arg	Val	Pro
			-25					-20					-15		
Leu	Ser	Asp	Ser	Trp	Ala	Leu	Leu	Pro	Ala	Ser	Ala	Gly	Val	Lys	Thr
		-10					-5					1			
Leu	Leu	Pro	Val	Pro	Ser	Phe	Glu	Asp	Val	Ser	Ile	Pro	Glu	Lys	Pro
5					10					15					20
Lys	Leu	Arg	Phe	Ile	Glu	Arg	Ala	Pro	Leu	Val	Pro	Lys	Val	Arg	Arg
			25					30					35		
Glu	Pro	Lys	Asn	Leu	Ser	Asp	Ile	Arg	Gly	Pro	Ser	Thr	Glu	Ala	Thr
			40					45					50		
Glu	Xaa	Thr	Glu	Gly	Asn	Phe	Ala	Ile	Leu	Ala	Leu	Gly	Gly	Gly	Tyr
		55					60					65			
Leu	His	Trp	Gly	His	Phe	Glu	Met	Met	Arg	Leu	Thr	Ile	Asn	Arg	Ser
	70					75					80				
Met	Asp	Pro	Lys	Asn	Met	Phe	Ala	Ile	Trp	Arg	Val	Pro	Ala	Pro	Phe
85					90					95					100

Lys	Pro	Ile	Thr	Arg	Lys	Ser	Val	Gly	His	Arg	Met	Gly	Gly	Gly	Lys
				105					110					115	
Gly	Ala	Ile	Asp	His	Tyr	Val	Thr	Pro	Val	Lys	Ala	Gly	Arg	Xaa	Xaa
			120					125					130		
Val	Glu	Met	Gly	Gly	Arg	Cys	Xaa	Phe	Glu	Glu	Val	Gln	Gly	Phe	Leu
		135					140					145			
Asp	Gln	Val	Ala	His	Lys	Leu	Pro	Phe	Ala	Ala	Lys	Ala	Val	Ser	Arg
	150					155					160				
Gly	Thr	Leu	Glu	Lys	Met	Arg	Lys	Asp	Gln	Glu	Glu	Arg	Glu	Xaa	Asn
165					170					175					180
Asn	Gln	Asn	Pro	Trp	Thr	Phe	Glu	Arg	Ile	Ala	Thr	Ala	Xaa	Met	Leu
				185					190					195	
Gly	Ile	Arg	Lys	Val	Leu	Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys
			200					205					210		
Xaa	Trp	Gly	Lys	Phe	Tyr	Met	Pro	Xaa	Arg	Val					
		215					220								

<210> 100
 <211> 77
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -30...-1
 <400> 100

Met	Leu	Arg	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe	Met
-30					-25					-20					-15
Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr	Leu	Thr
				-10				-5						1	
Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys	Cys	Leu	Ala
		5					10					15			
Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn	Pro	Ser	Gly	Pro
	20					25					30				
Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu	Val	Leu			
35					40					45					

<210> 101
 <211> 81
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -31...-1
 <400> 101

Met	Ser	Asn	Thr	His	Thr	Val	Leu	Val	Ser	Leu	Pro	His	Pro	His	Pro
-30						-25					-20				
Ala	Leu	Thr	Cys	Cys	His	Leu	Gly	Leu	Pro	His	Pro	Val	Arg	Ala	Pro
-15					-10					-5					1
Arg	Pro	Leu	Pro	Arg	Val	Glu	Pro	Trp	Asp	Pro	Arg	Trp	Gln	Asp	Ser
			5					10					15		
Glu	Leu	Arg	Tyr	Pro	Gln	Ala	Met	Asn	Ser	Phe	Leu	Asn	Glu	Arg	Ser
		20					25					30			
Ser	Pro	Cys	Arg	Thr	Leu	Arg	Gln	Glu	Ala	Ser	Ala	Asp	Arg	Cys	Asp
	35					40					45				
Leu															
50															

<210> 102

005750-0099950

Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
			135					140					145		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
		150					155					160			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	165					170					175				
Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser	Xaa	Lys	Gln
180					185					190					195
Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				200					205					210	
Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			215					220					225		

<210> 104
 <211> 158
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -37...-1
 <400> 104

Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro
		-35					-30					-25			
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
	-20					-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5					1			5						10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15					20					25			
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Arg	Ala	Asn	Ile	Val	Glu	Arg
	30					35					40				
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45				50					55					
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60				65					70						75
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
			80					85						90	
His	Thr	Gly	Pro	His	Gly	Gly	Ser	Ile	Gln	Gly	Met	Ser	Gly	Glu	Thr
		95					100						105		
Pro	Gly	Ser	Pro	Gln	Glu	Ala	Glu	Glu	Gly	Arg	Gly	Gly	Ser		
		110					115					120			

<210> 105
 <211> 51
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -19...-1
 <220>
 <221> UNSURE
 <222> 8
 <223> Xaa = any one of the twenty amino acids
 <400> 105

Met	Arg	Thr	Leu	Phe	Asn	Leu	Leu	Trp	Leu	Ala	Leu	Ala	Cys	Ser	Pro
			-15					-10					-5		
Val	His	Thr	Thr	Leu	Ser	Lys	Ser	Asp	Ala	Xaa	Lys	Pro	Pro	Gln	Arg

1 5 10
 Arg Cys Trp Arg Arg Val Ser Phe Gln Ile Ser Arg Cys Lys Thr Gly
 15 20 25
 Val Trp Trp
 30

<210> 106

<211> 359

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<220>

<221> UNSURE

<222> 20,64,65,130,156,282,288,289,294,296,300,302,310

<223> Xaa = any one of the twenty amino acids

<400> 106

Met	Leu	Leu	Ser	Ile	Gly	Met	Leu	Met	Leu	Ser	Ala	Thr	Gln	Val	Tyr
				-30					-25					-20	
Thr	Ile	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Leu	Leu	Pro	Val
			-15					-10					-5		
Glu	Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe
		1				5					10				
Asp	Asp	Leu	Pro	Ala	Xaa	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu
15					20					25					30
Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile
				35					40					45	
Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu
			50					55					60		
Ile	Xaa	Xaa	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln
		65					70					75			
Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp
	80					85					90				
Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	Glu	Val	Leu	Lys	Lys	Ile	Asp
95					100					105					110
Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp
				115					120					125	
Glu	Phe	Thr	Xaa	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe
			130					135					140		
Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Xaa	Val	Gly
		145					150					155			
Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Leu	Ser	Arg
	160					165					170				
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys
175					180					185					190
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys
				195					200					205	
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu
			210					215					220		
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr
		225					230					235			
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser
	240					245					250				
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu
255					260					265					270
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Xaa	Phe	Cys	Gln	Cys
				275					280					285	

Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly	Xaa	Pro	Ala	His	Xaa	Gln	Xaa
			290					295					300		
His	Asp	Arg	Ile	Ile	Gln	Thr	Xaa	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr
		305					310					315			
Asp	Ser	Ser	Asp	Ala	Glu	Glu									
	320					325									

<210> 107
 <211> 291
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -42...-1
 <400> 107

Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe
		-40					-35					-30			
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe
	-25					-20					-15				
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp
-10					-5				1				5		
Met	Cys	Leu	Lys	Ile	Ile	Lys	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg
			10					15					20		
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu
		25				30					35				
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val
	40					45					50				
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr
55					60					65					70
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser
				75					80					85	
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala
			90					95					100		
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile
		105					110					115			
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp
	120					125					130				
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys
135					140					145					150
Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala
				155					160					165	
Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu
			170					175						180	
Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu
		185					190					195			
Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val
	200					205					210				
Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile
215					220					225					230
Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro
				235					240					245	
Asn	Lys	Ala													

<210> 108
 <211> 67
 <212> PRT
 <213> Homo sapiens
 <220>

<221> SIGNAL

<222> -26...-1

<400> 108

Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
-25 -20 -15
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
-10 -5 1 5
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
10 15 20
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
25 30 35
Ile Cys Ser
40

<210> 109

<211> 127

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -63...-1

<400> 109

Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
-60 -55 -50
Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
-45 -40 -35
Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
-30 -25 -20
Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
-15 -10 -5 1
Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
5 10 15
Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu
20 25 30
Phe Ala Val Asn Phe Phe Val Gly Ala Ala Gly Ala Ser Gln Leu Phe
35 40 45
Arg Ile Trp Arg Tyr Asn Gln Glu Leu Lys Ala Lys Ala His Lys
50 55 60

<210> 110

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<220>

<221> UNSURE

<222> 53

<223> Xaa = any one of the twenty amino acids

<400> 110

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20 -15 -10 -5
Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys Gly Ala Cys Arg
1 5 10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
15 20 25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln

30		35		40
Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys Thr Lys Val Ala				
45		50		55
His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys Lys Gly Pro Trp				
	65		70	75

Ser

<210> 111

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 111

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly				
-20		-15		-10
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg				
	1		5	10
Ala Leu Val Asp Glu Thr Arg Met Gly Asn Cys Pro Gly Gly Pro Gln				
	15		20	25
Glu Asp His Ser Asp Gly Ile Phe Pro Asp Gln Ser Arg Trp Gln Pro				
	30		35	40
Val Ser Gly Gly Gly Ala Leu Cys Pro Leu Arg Gly Pro Pro His Arg				
45		50		55
Ala Ala Gly Gly Asp Met				60
	65			

<210> 112

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 112

Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala				
-25		-20		-15
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr				
	-5		1	5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu				
	10		15	20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val				
	25		30	35
Ser Gln Gln Glu Glu Leu Lys				
40		45		

<210> 113

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 113

Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala				
-40		-35		-30
Met Ser Ser Trp Ala Arg Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro				

005160-00999990

-25						-20						-15			
Ser	Leu	Pro	Gly	Ser	Pro	Val	Cys	Trp	Ala	Trp	Pro	Trp	Tyr	Pro	Asp
-10					-5					1				5	
Thr	Thr	Ser	Phe	Pro	Leu	Arg	Cys	Arg	Gly	Arg	Val				
			10					15							

<210> 114
 <211> 118
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -83...-1
 <220>
 <221> UNSURE
 <222> 28,32
 <223> Xaa = any one of the twenty amino acids

Met	Leu	Pro	Val	Gln	Ser	Phe	Thr	Leu	Val	Ala	Gln	Ala	Gly	Val	Gln
			-80					-75					-70		
Trp	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu	Phe	Lys	Gly
		-65					-60					-55			
Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro
	-50					-45					-40				
Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val	Glu	Thr	Gly	Leu	His
-35					-30					-25					-20
His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Ser	Cys	Ser	Pro	Pro
			-15					-10						-5	
Ala	Ser	Ala	Ser	Gln	Ser	Ala	Ala	Ile	Thr	Gly	Val	Ser	His	Val	Pro
			1			5						10			
Gly	Lys	Lys	Lys	Leu	Leu	Lys	Val	Glu	Lys	Lys	Asn	Leu	Arg	Xaa	Leu
	15					20					25				
Leu	Thr	Xaa	Ile	Lys	Thr										
30					35										

<210> 115
 <211> 76
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22...-1
 <220>
 <221> UNSURE
 <222> 22,43
 <223> Xaa = any one of the twenty amino acids

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
		-20					-15					-10			
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile
	-5					1				5					10
Lys	Gly	Trp	Ile	Pro	Trp	Ile	Gly	Val	Gly	Phe	Xaa	Phe	Gly	Lys	Ala
				15				20						25	
Pro	Leu	Glu	Phe	Ile	Glu	Lys	Ala	Arg	Ile	Lys	Val	Cys	Gly	Arg	Gly
			30					35					40		
Xaa	Arg	Gly	Leu	Gln	Arg	Arg	Gln	Cys	Phe	Leu	Phe				
		45					50								

<210> 116
 <211> 95
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -52...-1
 <400> 116

Met	Ala	Glu	Thr	Lys	Asp	Ala	Ala	Gln	Met	Leu	Val	Thr	Phe	Lys	Asp
		-50					-45					-40			
Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	Ala
	-35					-30					-25				
Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Val	Met	Leu	Glu	Thr	Cys	Gly	Leu	Leu
-20					-15					-10					-5
Val	Ser	Leu	Gly	Gln	Ser	Ile	Trp	Leu	His	Ile	Thr	Glu	Asn	Gln	Ile
			1				5					10			
Lys	Leu	Ala	Ser	Pro	Gly	Arg	Lys	Phe	Thr	Asn	Ser	Pro	Asp	Glu	Lys
	15						20					25			
Pro	Glu	Val	Trp	Leu	Ala	Pro	Gly	Leu	Phe	Gly	Ala	Ala	Ala	Gln	
	30					35					40				

<210> 117
 <211> 82
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22...-1
 <400> 117

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
		-20					-15					-10			
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile
	-5				1				5					10	
Lys	Gly	Trp	Ile	Pro	Trp	Ile	Gly	Val	Gly	Phe	Glu	Phe	Gly	Lys	Ala
			15				20						25		
Pro	Leu	Glu	Phe	Ile	Glu	Lys	Ala	Arg	Ile	Lys	Tyr	Gly	Pro	Ile	Phe
			30				35					40			
Thr	Val	Phe	Ala	Met	Gly	Asn	Arg	Met	Thr	Phe	Val	Thr	Glu	Glu	Gly
	45					50						55			
Arg	Asn														
	60														

<210> 118
 <211> 89
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -16...-1
 <400> 118

Met	Ile	Ile	Ser	Leu	Phe	Ile	Tyr	Ile	Phe	Leu	Thr	Cys	Ser	Asn	Thr
	-15					-10					-5				
Ser	Pro	Ser	Tyr	Gln	Gly	Thr	Gln	Leu	Gly	Leu	Gly	Leu	Pro	Ser	Ala
1			5					10					15		
Gln	Trp	Trp	Pro	Leu	Thr	Gly	Arg	Arg	Met	Gln	Cys	Cys	Arg	Leu	Phe
		20					25					30			
Cys	Phe	Leu	Leu	Gln	Asn	Cys	Leu	Phe	Pro	Phe	Pro	Leu	His	Leu	Ile
	35					40						45			

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 50 55 60
 Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 65 70

<210> 119
 <211> 30
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -19...-1
 <400> 119

Met Thr Met Ala Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala
 -15 -10 -5
 Leu Trp Ala Ala Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
 1 5 10

<210> 120
 <211> 115
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -103...-1
 <400> 120

Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
 -100 -95 -90
 Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
 -85 -80 -75
 Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
 -70 -65 -60
 Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro
 -55 -50 -45 -40
 Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp
 -35 -30 -25
 Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly
 -20 -15 -10
 Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg Cys Lys Gln Ser
 -5 1 5
 Ser Lys Pro
 10

<210> 121
 <211> 105
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -76...-1
 <400> 121

Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
 -75 -70 -65
 Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
 -60 -55 -50 -45
 Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
 -40 -35 -30
 Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Asn Leu

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005160:00999960

			-25					-20					-15			
Ile	Val	Tyr	Leu	Trp	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser	Ser	Ala	Asn	
		-10					-5					1				
Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro	Leu	Phe	Glu	
5					10					15					20	
Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser								
				25												

<210> 122
 <211> 93
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22...-1
 <400> 122

Met	Lys	Pro	Val	Leu	Pro	Leu	Gln	Phe	Leu	Val	Val	Phe	Cys	Leu	Ala	
		-20					-15					-10				
Leu	Gln	Leu	Val	Pro	Gly	Ser	Pro	Lys	Gln	Arg	Val	Leu	Lys	Tyr	Ile	
	-5					1			5						10	
Leu	Glu	Pro	Pro	Pro	Cys	Ile	Ser	Ala	Pro	Glu	Asn	Cys	Thr	His	Leu	
			15					20						25		
Cys	Thr	Met	Gln	Glu	Asp	Cys	Glu	Lys	Gly	Phe	Gln	Cys	Cys	Ser	Ser	
		30					35					40				
Phe	Cys	Gly	Ile	Val	Cys	Ser	Ser	Glu	Thr	Phe	Gln	Lys	Arg	Asn	Arg	
	45					50					55					
Ile	Lys	His	Lys	Gly	Ser	Glu	Val	Ile	Met	Pro	Ala	Asn				
	60					65					70					

<210> 123
 <211> 109
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -42...-1
 <400> 123

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala	
		-40					-35					-30				
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe	
	-25					-20					-15					
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Ala	Ile	Ile	
-10					-5				1					5		
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser	
		10					15					20				
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys	
	25					30					35					
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met	
	40				45					50						
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Gly	Val				
55					60					65						

<210> 124
 <211> 51
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL

0055300.091500

<222> -15...-1
 <400> 124
 Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
 -15 -10 -5 1
 Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
 5 10 15
 Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
 20 25 30
 Met Leu Val
 35

<210> 125
 <211> 56
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -27...-1
 <400> 125
 Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
 -25 -20 -15
 Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
 -10 -5 1 5
 Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
 10 15 20
 Trp Cys Ile Gln Pro Trp Ala Lys
 25

<210> 126
 <211> 162
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -21...-1
 <400> 126
 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
 -20 -15 -10
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 -5 1 5 10
 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
 15 20 25
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser
 30 35 40
 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
 45 50 55
 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
 60 65 70 75
 Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
 80 85 90
 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
 95 100 105
 Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
 110 115 120
 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
 125 130 135
 Arg Arg
 140

<210> 127
 <211> 126
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -68...-1
 <400> 127

Met	Ala	Ser	Ala	Ser	Ala	Arg	Gly	Asn	Gln	Asp	Lys	Asp	Ala	His	Phe
			-65					-60					-55		
Pro	Pro	Pro	Ser	Lys	Gln	Ser	Leu	Leu	Phe	Cys	Pro	Lys	Ser	Lys	Leu
		-50					-45					-40			
His	Ile	His	Arg	Ala	Glu	Ile	Ser	Lys	Ile	Met	Arg	Glu	Cys	Gln	Glu
	-35					-30				-25					
Glu	Ser	Phe	Trp	Lys	Arg	Ala	Leu	Pro	Phe	Ser	Leu	Val	Ser	Met	Leu
-20					-15				-10						-5
Val	Thr	Gln	Gly	Leu	Val	Tyr	Gln	Gly	Tyr	Leu	Ala	Ala	Asn	Ser	Arg
			1				5					10			
Phe	Gly	Ser	Leu	Pro	Lys	Val	Ala	Leu	Ala	Gly	Leu	Leu	Gly	Phe	Gly
	15					20					25				
Leu	Gly	Lys	Val	Ser	Tyr	Ile	Gly	Val	Cys	Gln	Ser	Lys	Phe	His	Phe
30						35				40					
Phe	Glu	Asp	Gln	Leu	Arg	Gly	Ala	Gly	Phe	Gly	Pro	Thr	Ala		
45					50				55						

<210> 128
 <211> 140
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -40...-1
 <400> 128

Met	Thr	Ser	Met	Thr	Gln	Ser	Leu	Arg	Glu	Val	Ile	Lys	Ala	Met	Thr
-40					-35					-30					-25
Lys	Ala	Arg	Asn	Phe	Glu	Arg	Val	Leu	Gly	Lys	Ile	Thr	Leu	Val	Ser
			-20						-15					-10	
Ala	Ala	Pro	Gly	Lys	Val	Ile	Cys	Glu	Met	Lys	Val	Glu	Glu	Glu	His
		-5					1				5				
Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly	Gly	Leu	Thr	Ala	Thr	Leu	Val
10						15				20					
Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu	Cys	Thr	Glu	Arg	Gly	Ala	Pro
25					30				35						40
Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr	Tyr	Met	Ser	Pro	Ala	Lys	Leu
				45					50					55	
Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His	Val	Leu	Lys	Gln	Gly	Lys	Thr
		60					65						70		
Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys	Leu
	75					80						85			
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn				
90						95					100				

<210> 129
 <211> 43
 <212> PRT
 <213> Homo sapiens
 <220>

005160:0099960

<221> SIGNAL

<222> -24...-1

<400> 129

Met	Gln	Cys	Phe	Ser	Phe	Ile	Lys	Thr	Met	Met	Ile	Leu	Phe	Asn	Leu
				-20					-15					-10	
Leu	Ile	Phe	Leu	Cys	Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp	Ser
			-5					1				5			
Pro	Tyr	Phe	Lys	Met	His	Lys	Pro	Val	Thr	Met					
	10					15									

<210> 130

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 130

Met	Trp	Trp	Phe	Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val
	-20					-15					-10				
Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr
-5					1				5					10	
Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr
			15					20					25		
Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala
		30					35					40			
Val	Leu	Cys	Gln	Lys											
	45														

<210> 131

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 131

Met	Ser	Pro	Gly	Ser	Ala	Leu	Ala	Leu	Leu	Trp	Ser	Leu	Pro	Ala	Ser
				-15					-10					-5	
Asp	Leu	Gly	Arg	Ser	Val	Ile	Ala	Gly	Leu	Trp	Pro	His	Thr	Gly	Val
			1				5					10			
Leu	Ile	His	Leu	Glu	Thr	Ser	Gln	Ser	Phe	Leu	Gln	Gly	Gln	Leu	Thr
	15					20					25				
Lys	Ser	Ile	Phe	Pro	Leu	Cys	Cys	Thr	Ser	Leu	Phe	Cys	Val	Cys	Val
30					35					40					45
Val	Thr	Val	Gly	Gly	Gly	Arg	Val	Gly	Ser	Thr	Phe	Val	Ala		
			50					55							

<210> 132

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 132

Met	Arg	Leu	Pro	Pro	Ala	Leu	Pro	Ser	Gly	Tyr	Thr	Asp	Ser	Thr	Ala
	-45						-40					-35			

005160 0092950

Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
-30 -25 -20
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
-15 -10 -5 1
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
5 10 15
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
20 25 30

<210> 133
<211> 53
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42...-1
<400> 133

Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
-40 -35 -30
Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
-25 -20 -15
Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
-10 -5 1 5
Met Cys Leu Lys Ile
10

<210> 134
<211> 1053
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 131..169
<223> Von Heijne matrix
score 4.19999980926514
seq MLAVSLTVPLLGA/MM
<220>
<221> polyA_site
<222> 1042..1053
<400> 134

gagcagatcg gacgggctgc gacagcgccg gccctgcgg ccgcaggctcg tcacagacga 60
tgatggccag gcccggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt 120
gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc 169
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
-10 -5
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa 217
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
1 5 10 15
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga 265
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
20 25 30
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata 313
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
35 40 45
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc 361
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val
50 55 60
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg 409

Val	Lys	Leu	Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser		
65					70					75					80		
ggc	cct	tgc	aaa	acc	cga	ggt	gat	gag	cct	gtg	tgt	ggg	aga	ccc	ctg		457
Gly	Pro	Cys	Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu		
				85				90						95			
ggt	atc	cgt	gca	ggg	ccc	aat	ggg	act	ctc	ttt	gtg	gcc	gat	gca	tac		505
Gly	Ile	Arg	Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr		
			100					105					110				
aag	gga	cta	ttt	gaa	gta	aat	ccc	tgg	aaa	cgt	gaa	gtg	aaa	ctg	ctg		553
Lys	Gly	Leu	Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu		
			115				120					125					
ctg	tcc	tcc	gag	aca	ccc	att	gag	ggg	aag	aac	atg	tcc	ttt	gtg	aat		601
Leu	Ser	Ser	Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn		
			130				135				140						
gat	ctt	aca	gtc	act	cag	gat	ggg	agg	aag	att	tat	ttc	acc	gat	tct		649
Asp	Leu	Thr	Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser		
					150					155					160		
agc	agc	aaa	tgg	caa	aga	cga	gac	tac	ctg	ctt	ctg	gtg	atg	gag	ggc		697
Ser	Ser	Lys	Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly		
				165				170						175			
aca	gat	gac	ggg	cgc	ctg	ctg	gag	tat	gat	act	gtg	acc	agg	gaa	gta		745
Thr	Asp	Asp	Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val		
			180					185					190				
aaa	gtt	tta	ttg	gac	cag	ctg	cgg	ttc	ccg	aat	gga	gtc	cag	ctg	tct		793
Lys	Val	Leu	Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser		
			195				200					205					
cct	gca	gaa	gac	ttt	gtc	ctg	gtg	gca	gaa	aca	acc	atg	gcc	agg	ata		841
Pro	Ala	Glu	Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile		
						215					220						
cga	aga	gtc	tac	gtt	tct	ggc	ctg	atg	aag	ggc	ggg	gct	gat	ctg	ttt		889
Arg	Arg	Val	Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe		
					230					235					240		
gtg	gag	aac	atg	cct	gga	ttt	cca	gac	aac	atc	cgg	ccc	agc	agc	tct		937
Val	Glu	Asn	Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser		
				245					250					255			
ggg	ggg	tac	tgg	gtg	ggc	atg	tcg	acc	atc	cgc	cct	aac	cct	ggg	ttt		985
Gly	Gly	Tyr	Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe		
				260				265					270				
tcc	atg	ctg	gat	ttc	tta	tct	gag	aga	ccc	tgg	att	aaa	agg	atg	att		1033
Ser	Met	Leu	Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile		
			275				280					285					
ttt	aag	gta	aaaaaaaaa	a													1053
Phe	Lys	Val															
			290														

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gtagcagtgg	ttcagcacac	tttggtatgt	tgactgtta	atg atg tac	gtt tct		114

005150-0095950

	Met	Met	Tyr	Val	Ser	
	1			5		
ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc						162
Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val						
	10		15		20	
tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa						210
Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys						
	25		30		35	
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg						258
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu						
	40		45		50	
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatgggtttat						306
Tyr Val Cys Val Phe Ile						
	55					
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca						366
tatttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga						426
tatttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg						486
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt						546
cagagaagaa catttaaagg gttaatatatt ttgaaacgtt ttcagataat atctatttga						606
ttattgtggc ttctatttga aatgtgtcta aaataaatgc tgttttattta aaatgaaaaa						666
aaaaaaaa						675
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<211> 1112						
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<213> Homo sapiens						
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score 4.80000019073486						
seq GVLLEPFVHQVGG/HS						
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<222> 1101..1112						
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ccgctggact ccgctgcctc ccccatctcc ccgccatctg cgcccggagg atg agc						116
				Met	Ser	
cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt						164
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu						
	-25		-20		-15	
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc						212
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg						
	-10		-5		1	5
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag						260
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln						
	10		15		20	
ttc tac gag acc ctc cct gct gag atg cgc aaa ttc tct ccc cag tac						308
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr						
	25		30		35	
aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat						356
Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu Pro His						
	40		45		50	
ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag gga agt gtg gcc						401

005160-0099950

Phe	Phe	Pro	Trp	Ser	Phe	Pro	Leu	Trp	Pro	Gln	Gly	Ser	Val	Ala	
55					60					65					
tgaatacccc	accccggtc	ctctgcaccc	agagctgggg	gccacctcag	aagtgtcatc										461
tctctctgag	cacgcattcc	cctgcagcag	tcgaggactg	agcagattga	gtgatgctgg										521
ggcagagagg	cctgagagga	aaggtgttca	gccagtcggt	tgtaaggcgc	tcgtcggcac										581
ctgctgaaac	gccccaccc	gacagcccca	tcctcaaaga	ctgtcttaac	tactcatggc										641
aggttctaga	gacttaaggg	gaaaagctgc	tttcaaggcc	accacatgtc	tgtgctcccc										701
aaccagctct	atctgccttg	tggttcatttt	gttattttgt	gacgtgagac	agcaaagacc										761
aataaaaaca	tattttataa	gaacaaaagg	cctgggtgcc	taccctgtgtg	ggggcactgt										821
gggaagcctt	tgctaggggtg	tcttgtgctg	tgtgggtttgt	tttgtttgcc	cctttatttt										881
gctttgctta	cccagctctc	ccttactctt	ggatgcttct	taaccctcag	gcaaacctgt										941
gttccccctg	tattcaggct	ctgcttttaa	gcaagccatg	aggctgttgg	agtttctgtt										1001
tagggcatta	aaaattcccc	caaactataa	agagcaatgt	tttcagtctt	ttaggattag										1061
aagaattaca	taaaaattaa	taaacatttt	caatgatgga	aaaaaaaaaa	a										1112

<210> 137
 <211> 547
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 359..454
 <223> Von Heijne matrix
 score 4
 seq FSFMLLGMGCLP/GF

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 <222> 536..547
 <400> 137

ctgggggagcc	ctgcctaaga	ctcatgctac	aagaagttaa	ataagtttcc	cgaagtcaca										60
cagctagcct	ctcatccctt	ttctactgag	aggaagtgga	atgcactccg	acaaggataa										120
ggttttattg	tgagctggcc	ttggaattaa	accaccacca	acacactttt	ggattatcag										180
aaggtggaag	gagtgcacaaa	atgtcattcc	catgcttgtc	tgccaggcaa	cctgggtgtcc										240
attctttatg	acgcctttcc	tgaatcacag	gtgcattggg	gtgcttcctc	ctccccagga										300
ctcccaccca	actttgtgaa	cacaacccac	ttagaggagt	tatctcagca	cattatga										358
atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct															406
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala															
-30		-25		-20											
ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct															454
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro															
-15		-10		-5											
gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc															502
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser															
1		5		10		15									
acc ttt gcc cat taaagtcaat tctccaccca taaaaaaaaa aaa															547
Thr Phe Ala His															
20															

<210> 138
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 <212> DNA
 <213> Homo sapiens
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 <221> sig_peptide
 <222> 26..316
 <223> Von Heijne matrix
 score 4
 seq RLPLVVSFIASSS/AN

005160-0099950

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<222> 1164..1169
<220>
<221> polyA_site
<222> 1187..1198
<400> 138
atcctgcgaa agaaggggggt tcatc atg gcg gat gac cta aag cga ttc ttg      52
                               Met Ala Asp Asp Leu Lys Arg Phe Leu
                               -95                               -90

tat aaa aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca      100
Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
                               -85                               -80                               -75

gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca      148
Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
                               -70                               -65                               -60

gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca      196
Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr
                               -55                               -50                               -45

gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt      244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys
                               -40                               -35                               -30                               -25

tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg      292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val
                               -20                               -15                               -10

gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc      340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser
                               -5                               1                               5

cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg      388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val
                               10                               15                               20

gaa gtt tct taatctgaca gtggtttcag tgtgtacctt atcttcatta      437
Glu Val Ser
25
taacaacaca atatcaatcc agcaatcttt agactacaat aatgcttttta tccatgtgct      497
caagaaaggg cccctttttc caacttatac taaagagcta gcatatagat gtaatttata      557
gatagatcag ttgctatatt ttctgggtgta ggggtctttct tattttagtga gatctaggga      617
taccacagaa atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat      677
ggatgagaga ttctattcag tggattagaa tcaaactggt acattgatcc acttgagccg      737
ttaagtgctg ccaattgtac aatatgccca ggcttgcaga ataaagccaa cttttttattg      797
tgaataataa taaggacata tttttcttca gattatgttt tatttctttg cattgagtga      857
ggtacataaa atggcttggg aaaagtaata aaatcagtac aatcactaac tttcctttgt      917
acatattatt ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg      977
ctgctcttta atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg      1037
taaccaatca gtgtttttaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat      1097
tctgtttcca atgttagtat gtatgtaaac atgatagtac agccattttt ttcatatgtg      1157
agtaaaaata aaatagtatt tttaaaagta aaaaaaaaaa a      1198

<210> 139
<211> 1400
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 36..107
<223> Von Heijne matrix
score 5.69999980926514
seq ILGLLGLLGTLVA/ML

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<220>
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<221> polyA_site
<222> 1389..1400
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cagtcctga agacgcttct actgagaggt ctgcc atg gcc tct ctt ggc ctc      53
                               Met Ala Ser Leu Gly Leu
                               -20
caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca ctg      101
Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr Leu
                               -15                               -10                               -5
gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt gcc      149
Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly Ala
                               1                               5                               10
agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa tgt      197
Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu Cys
15                               20                               25                               30
gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc ctt      245
Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu
                               35                               40                               45
ctg ggc ctg ccc gct gac atc cag gct gcc cag gcc atg atg gtg aca      293
Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr
                               50                               55                               60
tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc atg      341
Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met
                               65                               70                               75
aga tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg gcg      389
Arg Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala
                               80                               85                               90
gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc att      437
Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile
95                               100                               105                               110
cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca cca      485
Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
                               115                               120                               125
ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac ttg      533
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr Leu
                               130                               135                               140
ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc tgc      581
Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu Cys
                               145                               150                               155
ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc tac      629
Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala Tyr
                               160                               165                               170
caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa cct      677
Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln Pro
175                               180                               185                               190
ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat gtg      725
Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr Val
                               195                               200                               205
tgaagaacca ggggccagag ctgggggggtg gctgggtctg tgaaaaacag tggacagcac      785
cccgagggcc acaggtgagg gacactacca ctggatcgtg tcagaagggtg ctgctgaggg      845
tagactgact ttggccattg gattgagcaa aggcagaaat gggggctagt gtaacagcat      905
gcaggttgaa ttgccaagga tgctcgccat gccagccttt ctgttttctt caccttgctg      965
ctcccctgcc ctaagtcccc aaccctcaac ttgaaacccc attcccttaa gccaggactc      1025
agaggatccc tttgccctct ggtttacctg ggactccatc cccaaaccca ctaatcacat      1085

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cccactgact gaccctctgt gatcaaagac cctccctctg gctgagggtg gctcttagct 1145
cattgctggg gatgggaagg agaagcagtg gcttttgtgg gcattgctct aacctacttc 1205
tcaagcttcc ctccaaagaa actgattggc cctggaacct ccattcccact cttgttatga 1265
ctccacagtg tccagactaa tttgtgcatg aactgaaata aaaccatcct acggtatcca 1325
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aataaaaaaa aaaaa 1400

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<210> 140
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<222> 35..130
<223> Von Heijne matrix
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      seq VPMLLLIAGGSFG/LR
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<221> polyA_signal
<222> 505..510
<220>
<221> polyA_site
<222> 526..538
<400> 140

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                        Met Phe Ala Leu Ala Val Met
                        -30
cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg 103
Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu
-25                      -20                      -15                      -10
ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc 151
Leu Leu Ile Ala Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile
                        -5                      1                      5
cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa 199
Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys
      10                      15                      20
ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc 247
Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile
      25                      30                      35
tgt tgaagggcta ctatctttcc ttggcccttc tcccttggtg ggactcaatc 300
Cys
40
tccagactat ctccccagag aatcttgtca aggcttggct ttaagctttg ttgggaaaat 360
caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt gggaagatcc 420
tgacctcttc caaggaagaa atccagaaag ccttaagact aagacaactt gactctgctg 480
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<210> 141
<211> 1167
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 169..267
<223> Von Heijne matrix
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      seq LTFLFLHLPPSTS/LF
<220>

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005160-0999960

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<221> polyA_signal
<222> 1132..1137
<220>
<221> polyA_site
<222> 1155..1167
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tgcttttagta gtagtttaaa gtagtaactg ctactgtatt tagtggggtg gaattcagaa      120
gaaatttgaa gaccagatca tgggtggtct gcatgtgaat gaacagga atg agc cag      177
                                         Met Ser Gln
aca gcc tgg ctg tca ttg ctt tct tcc tcc cca ttt gga ccc ttc tct      225
Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly Pro Phe Ser
-30                               -25                               -20                               -15
gcc ctt aca ttt ttg ttt ctc cat cta cca cca tcc acc agt cta ttt      273
Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr Ser Leu Phe
                               -10                               -5                               1
att aac tta gca aga gga caa ata aag ggc cct ctt ggc ttg att ttg      321
Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly Leu Ile Leu
                    5                    10                    15
ctt ctt tct ttc tgt gga gga tat act aag tgc gac ttt gcc cta tcc      369
Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe Ala Leu Ser
                20                25                30
tat ttg gaa atc cct aac aga att gag ttt tct att atg gat cca aaa      417
Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met Asp Pro Lys
35                40                45                50
aga aaa aca aaa tgc taatgaagcc atcagtcaag ggtcacatgc caataaaca      472
Arg Lys Thr Lys Cys
                    55
taaattttcc agaagaaatg aaatccaact agacaaataa agtagagctt atgaaatggt      532
tcagtaagga tgagcttggt gttttttggt ttgttttggt ttgttttttt aaagacggag      592
tctcgctctg tcaactcaggc tggagtgcag tggatatgat ttggctcact gtaacctccg      652
cctcccgggt tcaagccatt ctctgcctc agtctcctga gtagctggga ttgcagggtgc      712
gtgccaccat gcctggctaa tttttgtggt tttggtagag acaggggttc accacgttgg      772
tcgggctggt ctggggtcc tgacctcttg atccgcctgc cttggcctcc caaagtgatg      832
ggattacaga tgtgagccac cgtgcctagc caaggatgag attttttaaag tatgttccag      892
ttctgtgtca tggttggaag acagagtagg aaggatatgg aaaagggtcat ggggaagcag      952
aggtgattca tggctctgtg aatttgaggt gaatgggtcc ttattgtcta ggccacttgt     1012
gaagaatatg agtcagttat tgccagcctt ggaatttact tctctagctt acaatggacc     1072
ttttgaactg gaaacacct tgtctgcatt cactttaaaa tgtcaaaact aatttttata     1132
ataaatgttt attttcacat cgaaaaaaa aaaaaa                                1167
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<210> 142
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<221> polyA_signal
<222> 697..702
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<221> polyA_site
<222> 721..730
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<221> misc_feature
<222> 1,14,28,52
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cttggtgaga gcgtgagctg ctgagatttg ggagtctgcg ctaggcccgc ttggagttct      120
gagccgatgg aagagttcac tc atg ttt gca ccc gcg gtg acg cgt gct ttt      172
                Met Phe Ala Pro Ala Val Thr Arg Ala Phe
                        -30                                -25
cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att      220
Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile
                -20                                -15                                -10
gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat      268
Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp
                -5                                1                                5                                10
gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag      316
Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu
                        15                                20                                25
aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag      364
Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys
                        30                                35                                40
ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat cct      412
Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro
                        45                                50                                55
gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca act      460
Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
                        60                                65                                70
tgactctgct gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt      520
cctaatatat acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg      580
ggtaatttga tgacaaataa tcttcactaa aggtcatgta cagggttttta tacttcccag      640
ctattccatc tgtggatgaa agtaacaatg ttggccacgt atattttaca cctcgaaata      700
aaaaatgtga atactgctcc aaaaaaaaaa      730

<210> 143
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<222> 108..170
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<221> polyA_site
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tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg      116
                                Met Trp Trp
                                -20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
                -15                                -10                                -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat      212

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Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His	
		1				5					10					
ata	gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggg	aca	gta	gct	cca	260
Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro	
15					20					25					30	
gaa	aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	ggt	tta	tgc	308
Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys	
				35					40						45	
att	gct	acc	att	tat	ggt	cgt	tat	aag	caa	ggt	cat	gct	ctg	agt	cct	356
Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro	
			50					55					60			
gaa	gag	aac	ggt	atc	atc	aaa	tta	aac	aag	gct	ggc	ctt	gta	ctt	gga	404
Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	
		65					70				75					
ata	ctg	agt	tgt	tta	gga	ctt	tct	att	gtg	gca	aac	ttc	cag	aaa	aca	452
Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr	
	80					85					90					
acc	ctt	ttt	gct	gca	cat	gta	agt	gga	gct	gtg	ctt	acc	ttt	ggg	atg	500
Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met	
95					100					105					110	
ggc	tca	tta	tat	atg	ttt	ggt	cag	acc	atc	ctt	tcc	tac	caa	atg	cag	548
Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln	
				115					120					125		
ccc	aaa	atc	cat	ggc	aaa	caa	gtc	ttc	tgg	atc	aga	ctg	ttg	ttg	ggt	596
Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val	
			130					135					140			
atc	tgg	tgt	gga	gta	agt	gca	ctt	agc	atg	ctg	act	tgc	tca	tca	ggt	644
Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val	
		145				150						155				
ttg	cac	agt	ggc	aat	ttt	ggg	act	gat	tta	gaa	cag	aaa	ctc	cat	tgg	692
Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp	
	160					165					170					
aac	ccc	gag	gac	aaa	ggg	tat	gcg	ctt	cac	atg	atc	act	act	gca	gca	740
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Ala	Leu	His	Met	Ile	Thr	Thr	Ala	Ala	
175					180					185					190	
gaa	tgg	tct	atg	tca	ttt	tcc	ttc	ttt	ggg	ttt	ttc	ctg	act	tac	att	788
Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr	Tyr	Ile	
				195					200					205		
cgt	gat	ttt	cag	aaa	att	tcc	tta	cgg	gtg	gaa	gcc	aac	tta	cat	gga	836
Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn	Leu	His	Gly	
			210					215					220			
tta	acc	ctc	tat	gac	act	gca	cct	tgc	cct	att	aac	aat	gaa	cga	aca	884
Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn	Glu	Arg	Thr	
		225				230					235					
cgg	cta	ctt	tcc	aga	gat	att	aga	tgaaaggata	aaatatttct	gtaatgatta						938
Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg									
	240					245										
tgattctcag	ggattgggga	aaggttcaca	gaagttgctt	attcttctct	gaaattttca											998
accacttaat	caaggctgac	agtaacactg	atgaatgctg	ataatcagga	aacatgaaag											1058
aagccatttg	atagattatt	ctaaaggata	tcatacaagaa	gactattaaa	aacacctatg											1118
cctatacttt	tttatctcag	aaaataaagt	caaaagacta	tgaaaaaaaa	aaaaaa											1174

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tcttcatctt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcacacctgs    120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct      180
aacagtcctat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca          232
                               Met Gly Cys Val Phe Gln Ser Thr
                               1               5
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
    10               15               20
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
    25               30               35               40
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu
               45               50               55
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag      424
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
               60               65               70
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
               75               80               85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
               90               95              100
caa atg ctt act taaagagggg ccaaggggca agagctttca tgtgcaagag      572
Gln Met Leu Thr
105
gcaaggaaac tgattatctt gagtaaattgc cagccttttg gctaagtact taccacagag      632
tgaatcttca aagaaatgan tcattaaatt atttcagrtc agaataaaaa takgagttat      692
tttagttaak aataaaatat tgataattat tgtattatta ctttaaacac acttccccct      752
cacaaaagcc ctgtgaagga tgttttgttc acatataatg tccaaatatg ttttggacac      812
atatttatta aatggaataa atagtamttg aaccctggca ccthtgacaa caaagtcyat      872
gttyttttta ctatgcccta ataccttttsa tcagttatcc acattgatgc tacatytgta      932
ttttataggt accctatggt aggtgttttg ggggatagaa aagaaataag cagkycaggc      992
tcagtggctc atgcctgtaa tcctagcatt ttgggaggct gaggcagcag aamtgcctga    1052
gccccagggt tcaagactgc agtgagctat gawggcacca ctgcattyta gcctgggwga    1112
cagagcaaga ctytgtttaa aataaaaaaa gagaaaaaaa aaaaaa                  1158

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      seq VCCYLFWLIAILA/QL
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09663600.091500

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      Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe
            -45                      -40                      -35
atc ccc aag ggt cct aac cgg gga gtt atc att acc atg ttg gtg acc      97
Ile Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr
      -30                      -25                      -20
tgt tca gtt tgc tgc tat ctc ttt tgg ctg att gca att ctg gcc caa      145
Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
      -15                      -10                      -5                      1
ctc aac cct ctc ttt gga ccg caa ttg aaa aat gaa acc atc tgg tat      193
Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
            5                      10                      15
ctg aag tat cat tgg cct tgaggaagaa gacatgctct acagtgtca      241
Leu Lys Tyr His Trp Pro
            20
gtcttttgagg tcacgagaag agaatgcctt ctagatgcaa aatcacctct aaaccagacc      301
acttttcttg acttgctgtg ttgggccatt agctgcctta aacgttaaca gcacatttga      361
atgccttatt ctacaatgca gcgtgttttc ctttgccttt ttgacacttt ggtgaattac      421
gtgcctccat aacctgaact gtgccgactc cacaaaacga ttatgtactc ttctgagata      481
gaagatgctg ttcttctgag agatacgtta ctctctcctt ggaatctgtg gatttgaaga      541
tggctcctgc cttctcacgt gggaatcagt gaagtgttta gaaactgctg caagacaaac      601
aagactccag tggggtggtc agtaggagag cacgttcaga gggaagagcc atctcaacag      661
aatcgcacca aactatactt tcaggatgaa tttcttcttt ctgccatctt ttggaataaa      721
tattttcttc ctttctatgt aaaaaaaaaa aaa      754

<210> 146
<211> 1073
<212> DNA
<213> Homo sapiens
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      seq PLSDSWALLPASA/GV
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<221> polyA_site
<222> 1060..1073
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cgctggggga gctccgcgcc gccggacgcc cgtgacc atg tgg agg ctg ctg gct      115
                        Met Trp Arg Leu Leu Ala
                                -25
cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg tca gat tcc tgg gca      163
Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu Ser Asp Ser Trp Ala
      -20                      -15                      -10
ctc ctc ccc gcc agt gct ggc gta aag aca ctg ctc cca gta cca agt      211
Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu Leu Pro Val Pro Ser
      -5                      1                      5                      10

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ttt gaa gat gtt tcc att cct gaa aaa ccc aag ctt aga ttt att gaa	259
Phe Glu Asp Val Ser Ile Pro Glu Lys Pro Lys Leu Arg Phe Ile Glu	
15 20 25	
agg gca cca ctt gtg cca aaa gta aga aga gaa cct aaa aat tta agt	307
Arg Ala Pro Leu Val Pro Lys Val Arg Arg Glu Pro Lys Asn Leu Ser	
30 35 40	
gac ata cgg gga cct tcc act gaa gct acg gag ttt aca gaa ggc aat	355
Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr Glu Phe Thr Glu Gly Asn	
45 50 55	
ttt gca atc ttg gca ttg ggt ggt ggc tac ctg cat tgg ggc cac ttt	403
Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr Leu His Trp Gly His Phe	
60 65 70	
gaa atg atg cgc ctg aca atc aac cgc tct atg gac ccc aag aac atg	451
Glu Met Met Arg Leu Thr Ile Asn Arg Ser Met Asp Pro Lys Asn Met	
75 80 85 90	
ttt gcc ata tgg cga gta cca gcc cct ttc aag ccc atc act cgc aaa	499
Phe Ala Ile Trp Arg Val Pro Ala Pro Phe Lys Pro Ile Thr Arg Lys	
95 100 105	
agt gtt ggg cat cgc atg ggg gga ggc aaa ggt gct att gac cac tac	547
Ser Val Gly His Arg Met Gly Gly Gly Lys Gly Ala Ile Asp His Tyr	
110 115 120	
gtg aca cct gtg aag gct ggc cgc ctt gtt gta gag atg ggt ggg cgt	595
Val Thr Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg	
125 130 135	
tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac cag gtt gcc cac aag	643
Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys	
140 145 150	
ttg ccc ttc gca gca aag gct gtg agc cgc ggg act cta gag aag atg	691
Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met	
155 160 165 170	
cga aaa gat caa gag gaa aga gaa cgt aac aac cag aac ccc tgg aca	739
Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr	
175 180 185	
ttt gag cga ata gcc act gcc aac atg ctg ggc ata cgg aaa gta ctg	787
Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu	
190 195 200	
agc cca tat gac ttg acc cac aag ggg aaa tac tgg ggc aag ttc tac	835
Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr	
205 210 215	
atg ccc aaa cgt gtg tagtgagtgt aggagataac tgtatatagg ctactgaaag	890
Met Pro Lys Arg Val	
220	
aaggattctg catttctatt cccctcagcc taccactga agtctttggg tagctcttaa	950
gccataacta aggagcagca tttgagtaga tttctgaaaa acgatgttat ttgttgattt	1010
aaaaagaaaa ctgtattttt attaaataaa atttaaacad cacttcagga aaaaaaaaaa	1070
aaa	1073

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<211> 413

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> 46..189

<223> Von Heijne matrix

score 4.09999990463257

seq VFMLIVSVLALIP/ET

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                                   Met Asp Asn Val
                                   -45
cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
               -40               -35               -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
               -25               -20               -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
               -10               -5               1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys
5               10               15               20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc      297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
               25               30               35
ggg cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
               40               45               50
taattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      402
aaaaaaaaaa a      413

<210> 148
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<222> 139..231
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      seq TCCHLGLPHPVRA/PR
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<221> polyA_site
<222> 598..609
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tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagttccgc ttgccagcag      120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt      171
               Met Ser Asn Thr His Thr Val Leu Val Ser Leu
               -30               -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac      219
Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His
-20               -15               -10               -5
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct      267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro
               1               5               10

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0051500-00953500-09563500

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agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc      315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe
      15                      20                      25
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg      363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser
      30                      35                      40
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta      411
Ala Asp Arg Cys Asp Leu
      45                      50
ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca      471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct      531
tcccacctcc ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg      591
agctgcaaaa aaaaaaaaaa      609

<210> 149
<211> 522
<212> DNA
<213> Homo sapiens
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<222> 512..522
<220>
<221> misc_feature
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<223> n=a, g, c or t
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gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt      110
      Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys
      1                      5                      10
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat      158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His
      15                      20                      25
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa      206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu
      30                      35                      40                      45
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa      254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys
      50                      55                      60
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta      302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu
      65                      70                      75
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag      350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu
      80                      85                      90
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt      398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val
      95                      100                      105
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca      446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser
      110                      115                      120                      125
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act      494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr
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Val Thr Ser Val Ser Thr
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005160-0099950

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ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag      170
      Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
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tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc      218
Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
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cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac      266
Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
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cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc      314
His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
      5                10                15
tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg      362
Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
      20                25                30
cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg      410
Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
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gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag      458
Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
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aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc      506
Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
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tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc      554
Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
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gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct      602
Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
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cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc      650
Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys
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ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg      698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val
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gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac      746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr
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gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa	842
Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys	
180 185 190	
caa gac gac ctc ctt tcg ggt gac ctc atc ttt ctg ggc tca gac agt	890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser	
195 200 205 210	
cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc	938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr	
215 220 225	
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Ile Leu	
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Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu	
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gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc	154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys	
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cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga	202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly	
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gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat	250
Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe Glu His	
15 20 25 30	
cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc aag gag	298
Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu Lys Glu	
35 40 45	
gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt gat cat	346
Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu Cys Asp His	
50 55 60	
cat gga gag aaa ctc cta ctc ttc tgt aag gag gat agg aaa gtc att	394
His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg Lys Val Ile	

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tgc	tgg	ctt	tgt	gag	cgg	tct	cag	gag	cac	cgt	ggt	cac	cac	aca	gtc		442
Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His	His	Thr	Val		
	80					85					90						
ctc	acg	gag	gaa	gta	ttc	aag	gaa	tgt	cag	gag	aaa	ctc	cag	gca	gtc		490
Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu	Gln	Ala	Val		
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ctc	aag	agg	ctg	aag	aag	gaa	gag	gag	gaa	gct	gag	aag	ctg	gaa	gct		538
Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys	Leu	Glu	Ala		
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Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val	Gln	Thr	Glu		
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Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser	Ile	Leu	Asn		
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aat	gag	gag	cag	aga	gag	ctg	caa	aga	ttg	gaa	gaa	gaa	gaa	aag	aag		682
Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu	Glu	Lys	Lys		
	160					165					170						
acg	ctg	gat	aag	ttt	gca	gag	gct	gag	gat	gag	cta	gtt	cag	cag	aag		730
Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val	Gln	Gln	Lys		
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cag	ttg	gtg	aga	gag	ctc	atc	tca	gat	gtg	gag	tgt	cgg	agt	cag	tggt		778
Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg	Ser	Gln	Trp		
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Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met	Lys	Trp	Ser		
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Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys	Lys	Leu	Lys		
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act	gta	ttc	cat	gct	cca	gat	ctg	agt	agg	atg	ctg	caa	atg	ttt	aga		922
Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln	Met	Phe	Arg		
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Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr	Leu	Asn	Ser		
	255				260					265				270			
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Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln	Arg	Gln	Val		
				275					280					285			
ata	tct	gtg	cca	att	tgg	cct	ttt	cag	tgt	tat	aat	tat	ggt	gtc	ttg		1066
Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr	Gly	Val	Leu		
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gga	tcc	caa	tat	ttc	tcc	tct	ggg	aaa	cat	tac	tgg	gaa	gtg	gac	gtg		1114
Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Val		
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tcc	aag	aaa	act	gcc	tgg	atc	ctg	ggg	gta	tac	tgt	aga	aca	tat	tcc		1162
Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg	Thr	Tyr	Ser		
			320			325					330						
cgc	cat	atg	aag	tat	gtt	gtt	aga	aga	tgt	gca	aat	cgt	caa	aat	ctt		1210
Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg	Gln	Asn	Leu		
					340					345					350		
tac	acc	aaa	tac	aga	cct	cta	ttt	ggc	tac	tgg	gtt	ata	ggg	tta	cag		1258
Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile	Gly	Leu	Gln		
				355					360					365			
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                               Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
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Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
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aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat      208
Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
                               10                               15                               20

aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag      256
Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
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agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac      304
Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
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aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc      352
Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser
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cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc      400
His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile
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tca ccc gtc tgg ctg cag ttg aag aga cgt ggc cgt gag atg ttt gag      448
Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu
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gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg      496
Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg
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aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac      544
Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp
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tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata      592
Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile
                               140                               145                               150

gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc      640
Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe
                               155                               160                               165

gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc      688
Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg
                               170                               175                               180

gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gcc ctg cac cag      736
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln
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200					205					210					215	
acc	gac	cag	ctg	ggc	atg	ttc	acg	cac	aag	gag	ttt	gag	cag	ctg	gcc	832
Thr	Asp	Gln	Leu	Gly	Met	Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	
				220					225					230		
ccc	gtg	ctg	gat	ggg	ttc	agc	ctc	atg	acc	tac	gac	tac	tct	aca	gcg	880
Pro	Val	Leu	Asp	Gly	Phe	Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	
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cat	cag	cct	ggc	cct	aat	gca	ccc	ctg	tcc	tgg	gtt	cga	gcc	tgc	gtc	928
His	Gln	Pro	Gly	Pro	Asn	Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	
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cag	gtc	ctg	gac	ccg	aag	tcc	aag	tgg	cga	agc	aaa	atc	ctc	ctg	ggg	976
Gln	Val	Leu	Asp	Pro	Lys	Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	
	265				270						275					
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Leu	Asn	Phe	Tyr	Gly	Met	Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	
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Leu	Gln	Val	Arg	Leu	Glu	Leu	Ala	Arg	Glu	Leu	Gly	Val	Gly	Val	Ser	
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Ile	Trp	Glu	Leu	Gly	Gln	Gly	Leu	Asp	Tyr	Phe	Tyr	Asp	Leu	Leu		
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Leu	Leu	Ser	Ile	Gly	Met	Leu	
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Val	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Pro	Leu	Pro	Val	Glu	
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gca	gac	att	tta	gca	tat	aac	ttt	gaa	aat	gca	tct	cag	aca	ttt	gat	203
Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe	Asp	
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gac	ctc	cct	gca	aga	ttt	ggg	tat	aga	ctt	cca	gct	gaa	ggg	tta	aag	251
Asp	Leu	Pro	Ala	Arg	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu	Lys	
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Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile	Val	
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Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu	Ile	
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Arg	Arg	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln	Arg	
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gca	gga	tac	aag	gca	gcc	ata	ggt	cac	aat	ggt	gat	tct	gat	gac	ctc	443
Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp	Leu	
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Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp	Glu	
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Phe	Thr	Tyr	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe	Ser	
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Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Ile	Val	Gly	Ile	
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tgt	ctc	atc	ttg	ata	gtc	att	ttc	atg	atc	aca	aaa	ttt	gtc	cag	gat	683
Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Phe	Val	Gln	Asp	
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aga	cat	aga	gct	aga	aga	aac	aga	ctt	cgt	aaa	gat	caa	ctt	aag	aaa	731
Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys	Lys	
			200					205					210			
ctt	cct	gta	cat	aaa	ttc	aag	aaa	gga	gat	gag	tat	gat	gta	tgt	gcc	779
Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys	Ala	
		215				220						225				
att	tgt	ttg	gat	gag	tat	gaa	gat	gga	gac	aaa	ctc	aga	atc	ctt	ccc	827
Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu	Pro	
	230					235					240					
tgt	tcc	cat	gct	tat	cat	tgc	aag	tgt	gta	gac	cct	tgg	cta	act	aaa	875
Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr	Lys	
	245				250					255					260	
acc	aaa	aaa	acc	tgt	cca	gtg	tgc	agg	caa	aaa	ggt	ggt	cct	tct	caa	923
Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser	Gln	
				265				270						275		
ggc	gat	tca	gac	tct	gac	aca	gac	agt	agt	caa	gaa	gaa	aat	gaa	gtg	971
Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu	Val	
			280				285						290			
aca	gaa	cat	acc	cct	tta	ctg	aga	cct	tta	gct	tct	gtc	agt	gcc	cag	1019
Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Ser	Val	Ser	Ala	Gln	
		295				300						305				
tca	ttt	ggg	gct	tta	tcg	gaa	tcc	cgc	tca	cat	cag	aac	atg	aca	gaa	1067

005T60-009E960

Ser	Phe	Gly	Ala	Leu	Ser	Glu	Ser	Arg	Ser	His	Gln	Asn	Met	Thr	Glu		
310						315					320						
tct	tca	gac	tat	gag	gaa	gac	gac	aat	gaa	gat	act	gac	agt	agt	gat		1115
Ser	Ser	Asp	Tyr	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr	Asp	Ser	Ser	Asp		
325					330					335					340		
gca	gaa	aat	gaa	att	aat	gaa	cat	gat	gtc	gtg	gtc	cag	ttg	cag	cct		1163
Ala	Glu	Asn	Glu	Ile	Asn	Glu	His	Asp	Val	Val	Val	Gln	Leu	Gln	Pro		
				345					350					355			
aat	ggt	gaa	cgg	gat	tac	aac	ata	gca	aat	act	ggt	tgacttttcag					1209
Asn	Gly	Glu	Arg	Asp	Tyr	Asn	Ile	Ala	Asn	Thr	Val						
				360				365									
aagatgattg	gtttattttcc	ctttaaaatg	attaggtata	tactgtaatt	tgatttttttg												1269
ctcccttaaa	agattttctgt	agaaataact	tatttttttag	tactctacag	tttaaatcaaa												1329
ttactgaaac	aggacttttg	atctggtatt	tatctgccaa	gaatatactt	cattcactaa												1389
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gccaaaacaa	aaaaaaaaa	a															1470

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gctgcctggt	cttcacactt	agctccaaac	ccatgaaaaa	ttgccaaagta	taaaagcttc												60
tcaagaatga	g	atg	gat	tct	agg	gtg	tct	tca	cct	gag	aag	caa	gat	aaa			110
	Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys				
				-40				-35					-30				
gag	aat	ttc	gtg	ggt	gtc	aac	aat	aaa	cgg	ctt	ggt	gta	tgt	ggc	tgg		158
Glu	Asn	Phe	Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp		
				-25				-20					-15				
atc	ctg	ttt	tcc	ctc	tct	ttc	ctg	ttg	gtg	atc	att	acc	ttc	ccc	atc		206
Ile	Leu	Phe	Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile		
			-10				-5					1					
tcc	ata	tgg	atg	tgc	ttg	aag	atc	att	agg	gag	tat	gaa	cgt	gct	ggt		254
Ser	Ile	Trp	Met	Cys	Leu	Lys	Ile	Ile	Arg	Glu	Tyr	Glu	Arg	Ala	Val		
	5				10				15								
gta	ttc	cgt	ctg	gga	cgc	atc	caa	gct	gac	aaa	gcc	aag	ggg	cca	ggt		302
Val	Phe	Arg	Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly		
	20			25				30						35			
ttg	atc	ctg	gtc	ctg	cca	tgc	ata	gat	gtg	ttt	gtc	aag	ggt	gac	ctc		350
Leu	Ile	Leu	Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu		
			40				45						50				
cga	aca	ggt	act	tgc	aac	att	cct	cca	caa	gag	atc	ctc	acc	aga	gac		398
Arg	Thr	Val	Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp		
			55				60						65				
tcc	gta	act	act	cag	gta	gat	gga	ggt	gtc	tat	tac	aga	atc	tat	agt		446
Ser	Val	Thr	Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser		
			70				75					80					
gct	gtc	tca	gca	gtg	gct	aat	gtc	aac	gat	gtc	cat	caa	gca	aca	ttt		494
Ala	Val	Ser	Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe		

85	90	95	
ctg ctg gct caa acc act	ctg aga aat gtc tta ggg aca cag acc ttg		542
Leu Leu Ala Gln Thr Thr	Leu Arg Asn Val Leu Gly Thr Gln Thr Leu		
100	105	110	115
tcc cag atc tta gct gga cga gaa gag atc gcc cat agc atc cag act			590
Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr			
120	125	130	
tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg			638
Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val			
135	140	145	
gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga tcc atg gca			686
Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala			
150	155	160	
gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc ctt gca gct			734
Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala			
165	170	175	
gaa gga gaa atg agt gct tcc aaa tcc ctg aag tca gcc tcc atg gtg			782
Glu Gly Glu Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val			
180	185	190	195
ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg cag acc ttg			830
Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu			
200	205	210	
agc acg gta gcc acc gag aag aat tct acg att gtg ttt cct ctg ccc			878
Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro			
215	220	225	
atg aat ata cta gag ggc att ggt ggc gtc agc tat gat aac cac aag			926
Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys			
230	235	240	
aag ctt cca aat aaa gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaa			982
Lys Leu Pro Asn Lys Ala			
245			

<210> 155
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 <213> Homo sapiens
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 <222> 425..430
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 <221> polyA_site
 <222> 443..455
 <400> 155

gtt atg cca ccc aga aac cta ctg gag tta ctt att aac atc aag gct	48
Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala	
1	5
gga acc tat ttg cct cag tcc tat ctg att cat gag cac atg gtt att	96
Gly Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile	
20	25
act gat cgc atc gaa aac att gat cac ctg ggt ttc ttt att tat cga	144
Thr Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg	
35	40
ctg tgt cat gac aag gaa act tac aaa ctg caa cgc aga gaa act att	192
Leu Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile	
50	55
aaa ggt att cag aaa cgt gaa gcc agc aat tgt ttc gca att cgg cat	240
Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His	
65	70
	75

005450-094500

ttt gaa aac aaa ttt gcc gtg gaa act tta att tgt tct tgaacagtca 289
Phe Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
80 85 90
agaaaaacat tattgaggaa aattaatatc acagcataac cccacccttt acattttgtg 349
cagtgattat tttttaaggt cttcttttcac gtaagtagca aacagggcctt tactatcttt 409
tcattctcatt aattcaatta aaaccattac cccaaaaaaa aaaaaa 455

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<222> 90..278
<223> Von Heijne matrix
score 3.5
seq GLVCAGLADMARP/AE
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<222> 704..709
<220>
<221> polyA_site
<222> 724..738
<400> 156

gggaaaagtg actagctccc cttcgttggtc agccagggac gagaacacag ccacgctccc 60
accggtgctgc caacgatccc tcggcggtgc atg tgc gcc gcc ggt gcc cga ggc 113
Met Ser Ala Ala Gly Ala Arg Gly
-60
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg 161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu
-55 -50 -45 -40
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca 209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr
-35 -30 -25
gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga 257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly
-20 -15 -10
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct 305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser
-5 1 5
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta 353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val
10 15 20 25
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg 401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly
30 35 40
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa 449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu
45 50 55
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct 500
Leu Lys Ala Lys Ala His Lys
60
agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa agcaaagcta 560
actgtgtggt tagaaggcac tgtaactggt agctagttct tgattcaata gaaaaatgca 620
gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta 680
acatttttct accatttggtc cgtaataaac catacttgct cgtaaaaaaa aaaaaaaa 738

<210> 157

<211> 649
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 <221> sig_peptide
 <222> 88..147
 <223> Von Heijne matrix
 score 12.3999996185303
 seq ALLLGALLGTAWA/RR
 <220>
 <221> polyA_signal
 <222> 619..624
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 <221> polyA_site
 <222> 637..649
 <400> 157
 ccaaagtgag agtccagcgg tcttccagcg cttggggccac ggcggcggcc ctgggagcag 60
 aggaggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg 114
 Met Lys Gly Trp Gly Trp Leu Ala Leu
 -20 -15
 ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 162
 Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
 -10 -5 1 5
 ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa 210
 Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
 10 15 20
 att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg 258
 Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
 25 30 35
 atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt 306
 Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val
 40 45 50
 ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgcttaaaa 359
 Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly
 55 60
 aggaccttgg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct 419
 catttggaag aagctgcagg cttattcccc atgcacttgc ttcctggctg caaaccttaa 479
 tactttgttt ctgctgtaga atttgttagc aaacaggagg tcttgatcag cacccttctc 539
 cacatccaca tgactggttt ttaatgtagc actgtggtat acatgcaaac atccgttcaa 599
 aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa 649

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 <223> Von Heijne matrix
 score 12.3999996185303
 seq ALLLGALLGTAWA/RR
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 <221> polyA_site
 <222> 703..714
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 agcagaggtg gagcgacccc attacgctaa ag atg aaa ggc tgg ggt tgg ctg 53
 Met Lys Gly Trp Gly Trp Leu
 -20 -15

gcc	ctg	ctt	ctg	ggg	gcc	ctg	ctg	gga	acc	gcc	tgg	gct	cgg	agg	agc	101
Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly	Thr	Ala	Trp	Ala	Arg	Arg	Ser	
			-10					-5					1			
cag	gat	ctc	cac	tgt	gga	gca	tgc	agg	gct	ctg	gtg	gat	gaa	cta	gaa	149
Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg	Ala	Leu	Val	Asp	Glu	Leu	Glu	
5					10					15						
tgg	gaa	att	gcc	cag	gtg	gac	ccc	aag	aag	acc	att	cag	atg	gga	tct	197
Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys	Lys	Thr	Ile	Gln	Met	Gly	Ser	
20				25						30					35	
ttc	cgg	atc	aat	cca	gat	ggc	agc	cag	tca	gtg	gtg	gag	gtg	cct	tat	245
Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln	Ser	Val	Val	Glu	Val	Pro	Tyr	
			40					45						50		
gcc	cgc	tca	gag	gcc	cac	ctc	aca	gag	ctg	ctg	gag	gag	ata	tgt	gac	293
Ala	Arg	Ser	Glu	Ala	His	Leu	Thr	Glu	Leu	Leu	Glu	Glu	Ile	Cys	Asp	
			55					60					65			
cgg	atg	aag	gag	tat	ggg	gaa	cag	att	gat	cct	tcc	acc	cat	cgc	aag	341
Arg	Met	Lys	Glu	Tyr	Gly	Glu	Gln	Ile	Asp	Pro	Ser	Thr	His	Arg	Lys	
		70					75					80				
aac	tac	gta	cgt	gta	gtg	ggc	cgg	aat	gga	gaa	tcc	agt	gaa	ctg	gac	389
Asn	Tyr	Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp	
85						90					95					
cta	caa	ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	437
Leu	Gln	Gly	Ile	Arg	Ile	Asp	Ser	Asp	Ile	Ser	Gly	Thr	Leu	Lys	Phe	
100					105					110					115	
gcg	tgt	ggg	agc	att	gtg	gag	gaa	tac	gag	gat	gaa	ctc	att	gaa	ttc	485
Ala	Cys	Gly	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe	
				120					125					130		
ttt	tcc	cga	gag	gct	gac	aat	gtt	aaa	gac	aaa	ctt	tgc	agt	aag	cga	533
Phe	Ser	Arg	Glu	Ala	Asp	Asn	Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg	
			135				140						145			
aca	gat	ctt	tgt	gac	cat	gcc	ctg	cac	ata	tcg	cat	gat	gag	cta		578
Thr	Asp	Leu	Cys	Asp	His	Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu		
		150					155					160				
tgaaccactg	gagcagccca	cactggcttg	atggatcacc	cccaggaggg	gaaaatggtg											638
gcaatgcctt	ttatatatta	tgtttttact	gaaattaact	gaaaaaatat	gaaacaaaa											698
gtacaaaaaa	aaaaaa															714

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 <221> sig_peptide
 <222> 33..107
 <223> Von Heijne matrix
 score 5
 seq MFAASLLAMCAGA/EV
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 <221> polyA_signal
 <222> 546..551
 <220>
 <221> polyA_site
 <222> 584..596
 <400> 159

cacagttcct	ctcctcctag	agcctgccga	cc	atg	ccc	gcg	ggc	gtg	ccc	atg	53					
				Met	Pro	Ala	Gly	Val	Pro	Met						
				-25					-20							
tcc	acc	tac	ctg	aaa	atg	ttc	gca	gcc	agt	ctc	ctg	gcc	atg	tgc	gca	101


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Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys Ala
      -15          -10          -5
ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata cct      149
Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile Pro
      1          5          10
gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga ctg      197
Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly Leu
15          20          25          30
aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt aaa      245
Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu Lys
      35          40          45
taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc ttaatttatt      305
gcatcaaact acttgctcctt aagcacttag tctaattgcta actgcaagag gaggtgctca      365
gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt tcttgaaaac      425
tgccaaagca catatcatca aaccatttca tgaatatggg ttggaagatg tttagtcttg      485
aatataacgc gaaatagaat atttgtaagt ctactatatg ggttgtcttt atttcatata      545
aattaagaaa ttattttaaaa ctatgaacta gtttcattaa aaaaaaaga a      596

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<210> 160
<211> 403
<212> DNA
<213> Homo sapiens
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<221> polyA_signal
<222> 375..380
<220>
<221> polyA_site
<222> 390..403
<400> 160

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tgaagagaat ggctgttgca gtcggcgctca gagcagctcc agtgccggggg attcggacgg      60
agagcgcgag gactcggcgcg ctgagcgcgcg cgcacagcag ctagaggcgcg tgctcaacaa      120
gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt      169
      Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe
      1          5          10          15
ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag      217
Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu
      20          25          30
ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg      265
Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu
      35          40          45
ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag      313
Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln
      50          55          60
agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc      363
Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu
      65          70
tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa      403

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<210> 161
<211> 727
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<213> Homo sapiens
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<222> 126..575
<223> Von Heijne matrix
      score 8.60000038146973
      seq LELLTSCSPASA/SQ

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<222> 670..675
<220>
<221> polyA_site
<222> 721..727
<220>
<221> misc_feature
<222> 257,376..377
<223> n=a, g, c or t
<400> 161
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60
gaccgggggt agggttttga gcccgtggga gctgccccac gcggcctcgt cctgccaacg      120
gtcggg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag      170
      Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
      -150                      -145                      -140
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-135                      -130                      -125                      -120
gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag      266
Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
      -115                      -110                      -105
ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga      314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
      -100                      -95                      -90
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc      362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
      -85                      -80                      -75
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc      410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
      -70                      -65                      -60
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac      458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
-55                      -50                      -45                      -40
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag      506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
      -35                      -30                      -25
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca      554
Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
      -20                      -15                      -10
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg      602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
      -5                      1                      5
agc cac cgt gcc cgg cag aga aaa act gct taagggtgaa aagagaaatt      652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala
10                      15
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga      712
agcaaaaaaa aaaaaa      727

<210> 162
<211> 944
<212> DNA
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<222> 90..155
<223> Von Heijne matrix
      score 5.90000009536743

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0051500-0093600-0966350

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seq IILGCLALFLLLQ/RK
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<400> 162
gaatcagggtt ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt      60
tctgcttctg gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg      113
                               Met Glu Leu Ile Ser Pro Thr Val
                               -20                               -15

att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag      161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys
                               -10                               -5                               1

aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga      209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly
                               5                               10                               15

gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca      257
Val Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala
                               20                               25                               30

aga atc aag gta tgt ggt cgt ggc aga cgg ggt ctc cag agg aga caa      305
Arg Ile Lys Val Cys Gly Arg Gly Arg Arg Gly Leu Gln Arg Arg Gln
35                               40                               45                               50

tgc ttt ctt ttt taaactttct ttcattgact cttaagtga gggctagaac      357
Cys Phe Leu Phe
acggggaaca tacctgcttg cctcaactaa aggatctagt catttctgaa ttcctctact      417
aacaattaac aacaatatcc tgtgcaaaat tttgcgaaag aaatgaaata caattgcagc      477
gtgcatcgac atttttggaa gtagagatta acttttcgta tttttacttc atcgaagtta      537
agttccaaat gtgtatgtgt taagtaaagt ttttcagtaa ttgggaaaga taaagtgtaa      597
tccaatttaa gtttgtgaaa atgagtaatt cgtatccaaa ttggagttaa caccaaagta      657
ttgtacaaat tgcttgacac gttggtccgt acacaataga caggctctgt atttttagct      717
gacgttggtta tttgatgatg atgtactcca ttttcactac ggcccgaaga gactagtaat      777
cctccttgta gtagatgttt ttgtcttgaa agtatctttt aaatgtctga gcactttaag      837
gaacagaccc ttattaatgt cttttaagtt ttattcaatt tccagtcaca aatattttat      897
ggtatttgat tgtctaataa atttgtatga tattaaaaaa aaaaaaa      944

<210> 163
<211> 598
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<223> Von Heijne matrix
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<222> 561..566
<220>
<221> polyA_site
<222> 587..598
<400> 163
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60
gacccgggggt agggttttga gcccggtggga gctgccccac gcggcctcgt cctgccaacg      120
gtcgg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      170
      Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys

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005150-009999

					-50					-45				-40		
gat	gtg	gct	gtg	acc	ttt	acc	cgg	gag	gag	tgg	aga	cag	ctg	gac	ctg	218
Asp	Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	
				-35				-30					-25			
gcc	cag	agg	acc	ctg	tac	cga	gag	gtg	atg	ctg	gag	acc	tgt	ggg	ctt	266
Ala	Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Val	Met	Leu	Glu	Thr	Cys	Gly	Leu	
			-20				-15				-10					
ctg	gtt	tca	cta	gtg	gaa	agc	att	tgg	ctg	cat	ata	aca	gaa	aac	cag	314
Leu	Val	Ser	Leu	Val	Glu	Ser	Ile	Trp	Leu	His	Ile	Thr	Glu	Asn	Gln	
	-5						1				5					
atc	aaa	ctg	gct	tca	cct	gga	agg	aaa	ttc	act	aac	tcg	cct	gat	gag	362
Ile	Lys	Leu	Ala	Ser	Pro	Gly	Arg	Lys	Phe	Thr	Asn	Ser	Pro	Asp	Glu	
10					15				20				25			
aag	cct	gag	gtg	tgg	ttg	gct	cca	ggc	ctg	ttc	ggg	gcc	gca	gcc	cag	410
Lys	Pro	Glu	Val	Trp	Leu	Ala	Pro	Gly	Leu	Phe	Gly	Ala	Ala	Ala	Gln	
					30				35				40			
tgacg	ccatc	aaggat	gtct	tggtt	tctctg	ttcctt	tcttc	ttggtt	cagg	cttctg	attg					470
tcctc	aggct	ggctc	ctcat	agggat	gctg	gggtg	ctgcag	ccttg	actgg	ggcag	caggc					530
ccccat	gttc	aatccat	cct	cccac	cttg	aataa	atgct	ttcttt	tcac	aatgag	aaaaa					590
aaaaaaaa																598
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ttctg	gaagg	tgctgg	acaa	aaac	atg	gaa	cta	att	tcc	cca	aca	gtg	att			111
						Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile		
							-20					-15				
ata	atc	ctg	ggt	tgc	ctt	gct	ctg	ttc	tta	ctc	ctt	cag	cgg	aag	aat	159
Ile	Ile	Leu	Gly	Cys	Leu	Ala	Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	
			-10				-5				1					
ttg	cgt	aga	ccc	ccg	tgc	atc	aag	ggc	tgg	att	cct	tgg	att	gga	gtt	207
Leu	Arg	Arg	Pro	Pro	Cys	Ile	Lys	Gly	Trp	Ile	Pro	Trp	Ile	Gly	Val	
5					10				15							
gga	ttt	gag	ttt	ggg	aaa	gcc	cct	cta	gaa	ttt	ata	gag	aaa	gca	aga	255
Gly	Phe	Glu	Phe	Gly	Lys	Ala	Pro	Leu	Glu	Phe	Ile	Glu	Lys	Ala	Arg	
20				25				30					35			
atc	aag	tat	gga	cca	ata	ttt	aca	gtc	ttt	gct	atg	gga	aac	cga	atg	303
Ile	Lys	Tyr	Gly	Pro	Ile	Phe	Thr	Val	Phe	Ala	Met	Gly	Asn	Arg	Met	
			40				45				50					
acc	ttt	gtt	act	gaa	gaa	gaa	gga	att	aat	gtg	ttt	cta	aaa	tcc		348
Thr	Phe	Val	Thr	Glu	Glu	Glu	Gly	Ile	Asn	Val	Phe	Leu	Lys	Ser		
			55				60				65					
aaaaaaaa	aa															360
<210> 165																
<211> 490																

005160-00969960

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<212> DNA
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<221> sig_peptide
<222> 77..124
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      score 4.80000019073486
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<221> polyA_signal
<222> 461..466
<220>
<221> polyA_site
<222> 477..490
<400> 165
atgagcttcc agccccaaga gtggaggctg ccacatccca acatagtatc tattgaaaag      60
gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca      112
              Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
              -15              -10              -5
tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt      160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
              1              5              10
ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc      208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
              15              20              25
tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc      256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
              30              35              40
ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc      304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
45              50              55              60
tgg gac tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact      353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
              65              70
gtcttccttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct      413
cccttgccct ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa      473
gtgaaaaaaaa aaaaaaa      490

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<210> 166
<211> 488
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 458..463
<220>
<221> polyA_site
<222> 475..488
<400> 166
ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac      55
              Met Lys Val Asp Lys Asp
              1              5
cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag      103
Arg Gln Met Val Val Leu Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu
              10              15              20
gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac      151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr
              25              30              35

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005160-0099950

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agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt      199
Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys
    40                                45                                50
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg      247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met
55                                60                                65                                70
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag      295
Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys
                                75                                80                                85
gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa      343
Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln
                                90                                95                                100
gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga      394
Glu Lys Leu Ser Phe Phe Arg
    105
tgtctgagtc ctcaaggtga ctggggactt ggaacccta ggacctgaac aaccaagact      454
ttaaataaat tttaaaatgc aaaaaaaaaa aaaa                                488

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<210> 167
<211> 771
<212> DNA
<213> Homo sapiens
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<222> 48..356
<223> Von Heijne matrix
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      seq VYAFLGLTAPSGS/KE
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<221> polyA_signal
<222> 742..747
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<222> 760..771
<400> 167

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ccacagccct tttcaggacc caaacaaccg cagccgctgt tcccagg atg gtg atc      56
                                Met Val Ile
cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa      104
Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys
-100                                -95                                -90                                -85
caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa      152
Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu
                                -80                                -75                                -70
gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa      200
Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu
                                -65                                -60                                -55
aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct      248
Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro
                                -50                                -45                                -40
cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt      296
Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe
                                -35                                -30                                -25
gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc      344
Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala
-20                                -15                                -10                                -5
cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca      389
Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala
    1                                5                                10

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aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa

959

<210> 169
<211> 464
<212> DNA
<213> Homo sapiens
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<223> Von Heijne matrix
score 9.80000019073486
seq LVVFCLALQLVPG/SP

<220>
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<222> 437..442
<220>
<221> polyA_site
<222> 455..464
<400> 169

gccagaactt actcaccat cccactgaca cc atg aag cct gtg ctg cct ctc 53
Met Lys Pro Val Leu Pro Leu
-20

cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt 101
Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser
-15 -10 -5 1

ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata 149
Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile
5 10 15

tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc 197
Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys
20 25 30

gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca 245
Glu Lys Gly Phe Gln Cys Cys Ser Ser Phe Cys Gly Ile Val Cys Ser
35 40 45

tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa 293
Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu
50 55 60 65

gtc atc atg cct gcc aac tgaggcatat ttcctagatc attttgcctc 341
Val Ile Met Pro Ala Asn
70

tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc 401
caatatctaa cctgcaaadc gtttttgagt ttggcaataa aggctaactt accaaaaaaa 461
aaa 464

<210> 170
<211> 799
<212> DNA
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<223> Von Heijne matrix
score 5.19999980926514
seq LLFDLVCHEFCQS/DD

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<221> polyA_site

<222> 787..799

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agctgccaaa caagtacgtt ctgaaaatcc agaatggctt gatgtttac atg cac att 118

Met His Ile

-40

tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat 166

Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His

-35

-30

-25

tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc 214

Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val

-20

-15

-10

tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa 262

Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu

-5

1

5

cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat 310

Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr

10 15 20 25

gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt 358

Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu

30

35

40

cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt 406

Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys

45

50

55

cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa 454

Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys

60

65

70

agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat 502

Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp

75

80

85

att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag 550

Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu

90 95 100 105

acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt 598

Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys

110

115

120

tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa 646

Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu

125

130

135

gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac 694

Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp

140

145

150

ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga 740

Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155

160

165

attggaatta cttctgtaca agaaataaac tttattttttc tcactgaaaa aaaaaaaaaa 799

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<211> 320

<212> DNA

<213> Homo sapiens

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<221> polyA_site

<222> 308..320

<400> 171

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Met Pro His Ser Lys Pro

005160-009E9960

ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt	103
Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe	
10 15 20	
cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta	151
Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu	
25 30 35	
aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc	199
Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu	
40 45 50	
ggg gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggt	254
Gly Val Phe Asn Leu	
55	
tggttgagg actgagtgtg tggaagtttt tcataaactt tggatgctag tgtaaaaaaa	314
aaaaaa	320

<210> 172
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 <212> DNA
 <213> Homo sapiens
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 <222> 129..209
 <223> Von Heijne matrix
 score 4.90000009536743
 seq CLLSYIALGAIHA/KI

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<222> 318..331	
<400> 172	
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cacctctagc ctgctcattt ccagctcaga aattctacta atggcgtttt ttcttcctga	120
aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc	170
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile	
-25 -20 -15	
tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt	218
Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys	
-10 -5 1	
agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg	266
Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val	
5 10 15	
aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc	316
Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys	
20 25	
caaaaaaaaa aaaaa	331

<210> 173
 <211> 1075
 <212> DNA
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 <221> sig_peptide
 <222> 78..359
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 score 4.19999980926514
 seq IILTAVYFALSIS/LH
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 <221> polyA_signal

seq LPFSLVSMMLVTQG/LV

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<222> 621..632
<400> 174
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c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt      109
  Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
      -65                      -60                      -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
      -50                      -45                      -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
      -35                      -30                      -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
      -20                      -15                      -10                      -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga      301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
      1                      5                      10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc      349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
      15                      20                      25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt      397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
      30                      35                      40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg      445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
      45                      50                      55                      60
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt      493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
      65                      70                      75
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact      543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
      80                      85
ttcgaagttt tttaaaccctc tgaatttgta cacatttaaa atttcaagtg tacttttaaaa      603
taaaataactt ctaatgtaaa aaaaaaaaaa      632

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<210> 175
<211> 430
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 402..407
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<221> polyA_site
<222> 419..430
<400> 175
gtattgggaa agtgatttgt gaa atg aaa gta gaa gaa gag cat acc aat gca      53
      Met Lys Val Glu Glu Glu His Thr Asn Ala
      1                      5                      10
ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata      101
Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile

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	15	20	25	
tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt				149
Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser				
	30	35	40	
gtc gat atg aac ata acg tac atg tca cct gca aaa tta gga gag gat				197
Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp				
	45	50	55	
ata gtg att aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt				245
Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe				
	60	65	70	
acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta ata gca caa				293
Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln				
	75	80	85	90
gga aga cac aca aaa cac ctg gga aac tgagagaaca gcagaatgac				340
Gly Arg His Thr Lys His Leu Gly Asn				
	95			
ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg				400
aaataaacta gcaaaaccaa aaaaaaaaaa				430

<210> 176

<211> 185

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 42..113

<223> Von Heijne matrix

score 3.70000004768372

seq ILFNLLIFLCGFT/NY

<220>

<221> polyA_site

<222> 172..185

<400> 176

ctttcagaac tcactgccaa gagccctgaa caggagccac c atg cag tgc ttc agc	56
Met Gln Cys Phe Ser	
	-20

ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt	104
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys	
	-15

ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg	152
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met	
	1
	5
	10

cat aaa cct gtt aca atg taataaaaaaa aaaaa	185
His Lys Pro Val Thr Met	
	15

<210> 177

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 108..170

<223> Von Heijne matrix

score 5.5

seq SFLPSALVIWTSA/AF

<220>

<221> polyA_signal

<222> 550..555

<220>

<221> polyA_site

<222> 574..585

<400> 177

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cacgttcttg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc      60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg      116
                                   Met Trp Trp
                                   -20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
                                   -15               -10               -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat      212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
                                   1               5               10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca      260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15                20                25                30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt      308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
                                   35                40                45
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa      364
Gln Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt      424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg      484
gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaa      544
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa a      585

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<210> 178

<211> 613

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 118..171

<223> Von Heijne matrix

score 5.90000009536743

seq ALALLWSLPASDL/GR

<220>

<221> polyA_signal

<222> 583..588

<220>

<221> polyA_site

<222> 602..613

<400> 178

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gggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg      60
gagctgccgc acagagcctg gtgtccacaa gcttccaggt tggggttgga gcctggg      117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct      165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
                                   -15               -10               -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt      213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
                                   1               5               10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc      261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
15                20                25                30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt      309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val

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	35	40	45	
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca				351
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala				
	50	55	60	
tgagtcgatg ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg				411
tcgaaaataa gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt				471
attgattaag ttactgtaaa agcttggggt tattttttgta ggacttaatg gctaagaatt				531
agaacatagc aaggggggtc ctctgttgga gtaatgtaaa ttgtaattat aaataaacat				591
gcaaaccctt aaaaaaaaaa aa				613

<210> 179
 <211> 427
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 128..268
 <223> Von Heijne matrix
 score 5.5
 seq SALLFFARPCVFC/FK
 <220>
 <221> polyA_signal
 <222> 410..415
 <220>
 <221> polyA_site
 <222> 424..427
 <400> 179

agcttggatt tacactgggc aacgtgggtg gaatgtatct ggctcagaac tatgatatac	60
caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaaag aagaaacccc	120
ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct	169
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser	
-45 -40 -35	
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt	217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe	
-30 -25 -20	
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt	265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe	
-15 -10 -5	
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca	313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr	
1 5 10 15	
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg	361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly	
20 25 30	
agg ttc taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa	417
Arg Phe	
aaaaacaaaa	427

<210> 180
 <211> 905
 <212> DNA
 <213> Homo sapiens
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 <222> 149..457
 <223> Von Heijne matrix
 score 4.90000009536743
 seq FLLAQTTLRNVLG/TQ


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<220>
<221> polyA_site
<222> 893..912
<400> 180
gctgcctggt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc      60
tcaagaatga gatggattct aggggtgtctt cacctgagaa gcaagataaa gagaatttcg      120
tgggtgtcaa caataaacgg cttggtgt atg tgg ctg gat cct gtt ttc cct      172
                               Met Trp Leu Asp Pro Val Phe Pro
                               -100
ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg      220
Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
-95                               -90                               -85                               -80
ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa      268
Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
                               -75                               -70                               -65
gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc      316
Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
                               -60                               -55                               -50
acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga      364
Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
-45                               -40                               -35
atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa      412
Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln
-30                               -25                               -20
gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca      460
Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr
-15                               -10                               -5                               1
cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc      508
Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser
5                               10                               15
atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg      556
Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val
20                               25                               30
gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga      604
Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg
35                               40                               45
tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc      652
Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val
50                               55                               60                               65
ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc      700
Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala
70                               75                               80
tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg      748
Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu
85                               90                               95
cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt      796
Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe
100                               105                               110
cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat      844
Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp
115                               120                               125
aac cac aag aag ctt cca aat aaa gcc tgagggtcctc ttgcggtagt      891
Asn His Lys Lys Leu Pro Asn Lys Ala
130                               135
caaaaaaaaaaaaaa      905

<210> 181
<211> 307

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005760-099950

<212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -13...-1
 <400> 181
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
 -10 -5 1
 Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
 Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
 20 25 30 35
 Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50
 Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
 55 60 65
 Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
 70 75 80
 Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
 85 90 95
 Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr Lys Gly Leu
 100 105 110 115
 Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
 120 125 130
 Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
 135 140 145
 Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
 150 155 160
 Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp
 165 170 175
 Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
 180 185 190 195
 Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
 200 205 210
 Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
 215 220 225
 Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
 230 235 240
 Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
 245 250 255
 Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
 260 265 270 275
 Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Val
 280 285 290
 Lys Lys Lys

<210> 182
 <211> 59
 <212> PRT
 <213> Homo sapiens
 <400> 182
 Met Met Tyr Val Ser Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu
 1 5 10 15
 Phe Asp Tyr Val Val Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu
 20 25 30
 Lys Gln Leu Lys Lys Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys
 35 40 45
 Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile

50

55

<210> 183

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 183

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
			-25					-20					-15		
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val
		-10					-5					1			
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu
5					10					15					20
His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ala	Glu	Met	Arg	Lys	Phe	Ser	Pro
			25						30					35	
Gln	Tyr	Lys	Gly	Gln	Ser	Gln	Arg	Pro	Leu	Val	Ser	Trp	Pro	Ser	Leu
			40				45						50		
Pro	His	Phe	Phe	Pro	Trp	Ser	Phe	Pro	Leu	Trp	Pro	Gln	Gly	Ser	Val
		55					60					65			
Ala															

<210> 184

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32...-1

<400> 184

Met	Leu	Gly	Thr	Thr	Gly	Leu	Gly	Thr	Gln	Gly	Pro	Ser	Gln	Gln	Ala
		-30					-25					-20			
Leu	Gly	Phe	Phe	Ser	Phe	Met	Leu	Leu	Gly	Met	Gly	Gly	Cys	Leu	Pro
	-15					-10					-5				
Gly	Phe	Leu	Leu	Gln	Pro	Pro	Asn	Arg	Ser	Pro	Thr	Leu	Pro	Ala	Ser
1				5					10					15	
Thr	Phe	Ala	His												
			20												

<210> 185

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -97...-1

<400> 185

Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe	Leu	Tyr	Lys	Lys	Leu	Pro	Ser	Val
		-95					-90					-85			
Glu	Gly	Leu	His	Ala	Ile	Val	Val	Ser	Asp	Arg	Asp	Gly	Val	Pro	Val
	-80					-75					-70				
Val	Lys	Val	Ala	Asn	Asp	Asn	Ala	Pro	Glu	His	Ala	Leu	Arg	Pro	Gly
-65				-60					-55					-50	
Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly
			-45					-40					-35		
Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val

005150-0099960

			-30					-25					-20			
Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser	
		-15					-10					-5				
Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro	
1					5					10					15	
Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser					
				20					25							

<210> 186
 <211> 230
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -24...-1
 <400> 186

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Leu	
				-20					-15					-10		
Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	Lys	Thr	
			-5					1				5				
Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	Phe	Ser	Lys	
10						15					20					
Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	Ile	Thr	Gln	Cys	
25					30					35					40	
Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	Asp	Ile	Gln	Ala	Ala	
				45					50					55		
Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile	
			60					65					70			
Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg	
		75				80					85					
Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	
	90					95					100					
Gly	Leu	Leu	Gly	Phe	Ile	Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	
105					110					115					120	
Arg	Asp	Phe	Tyr	Ser	Pro	Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	
				125					130					135		
Gly	Glu	Ala	Leu	Tyr	Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	
			140					145					150			
Ala	Gly	Ile	Ile	Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	
		155				160					165					
Asn	Tyr	Tyr	Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	
	170					175					180					
Pro	Arg	Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	
185					190					195					200	
Ser	Leu	Thr	Gly	Tyr	Val											
				205												

<210> 187
 <211> 72
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1
 <400> 187

Met	Phe	Ala	Leu	Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu	
		-30					-25					-20				
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Ala	Gly	Gly	Ser	Phe	Gly	

005160-0093960

-15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Gly Ser Ile Cys
 35 40

<210> 188
 <211> 88
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -33...-1
 <400> 188

Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly
 -30 -25 -20
 Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr
 -15 -10 -5
 Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly
 1 5 10 15
 Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe
 20 25 30
 Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met
 35 40 45
 Asp Pro Lys Arg Lys Thr Lys Cys
 50 55

<210> 189
 <211> 106
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1
 <400> 189

Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 190
 <211> 267
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL

005160-0091500

<222> -21...-1

<400> 190

Met	Trp	Trp	Phe	Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val
-20						-15					-10				
Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr
-5					1				5					10	
Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr
			15					20				25			
Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala
		30					35					40			
Val	Leu	Cys	Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala
	45					50					55				
Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu
60					65					70					75
Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe
				80					85					90	
Gln	Lys	Thr	Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr
			95					100						105	
Phe	Gly	Met	Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr
		110					115					120			
Gln	Met	Gln	Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu
	125					130					135				
Leu	Leu	Val	Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys
140					145					150					155
Ser	Ser	Val	Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys
				160					165					170	
Leu	His	Trp	Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Ala	Leu	His	Met	Ile	Thr
			175					180					185		
Thr	Ala	Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu
		190					195					200			
Thr	Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
	205					210					215				
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn
220					225					230					235
Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg					
				240					245						

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<212> PRT

<213> Homo sapiens

<400> 191

Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile
1				5					10					15	
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu
			20					25					30		
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg
		35					40					45			
Val	His	Leu	Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu
	50					55					60				
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg
65					70					75					80
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val
				85					90					95	
Leu	Pro	Glu	Glu	Pro	Lys	Gly	Thr	Gln	Met	Leu	Thr				
			100					105							

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Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe	Ser
			-45					-40					-35		
Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Asp	Ile	Ile	Asn	Ser	Leu
		-30					-25					-20			
Val	Thr	Thr	Val	Phe	Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro
	-15					-10					-5				
Glu	Thr	Thr	Thr	Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr
1				5					10					15	
Ala	Val	Cys	Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu
			20					25					30		
Phe	Asn	Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys
		35					40					45			
Glu	Val	Leu													
		50													

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Met	Ser	Asn	Thr	His	Thr	Val	Leu	Val	Ser	Leu	Pro	His	Pro	His	Pro
	-30					-25					-20				
Ala	Leu	Thr	Cys	Cys	His	Leu	Gly	Leu	Pro	His	Pro	Val	Arg	Ala	Pro
-15					-10					-5					1
Arg	Pro	Leu	Pro	Arg	Val	Glu	Pro	Trp	Asp	Pro	Arg	Trp	Gln	Asp	Ser
		5						10					15		
Glu	Leu	Arg	Tyr	Pro	Gln	Ala	Met	Asn	Ser	Phe	Leu	Asn	Glu	Arg	Ser
		20				25						30			
Ser	Pro	Cys	Arg	Thr	Leu	Arg	Gln	Glu	Ala	Ser	Ala	Asp	Arg	Cys	Asp
	35					40					45				
Leu															
50															

<210> 196
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<400> 196

Met	Lys	Val	His	Met	His	Thr	Lys	Phe	Cys	Leu	Ile	Cys	Leu	Leu	Thr
1			5						10					15	
Phe	Ile	Phe	His	His	Cys	Asn	His	Cys	His	Glu	Glu	His	Asp	His	Gly
			20					25					30		
Pro	Glu	Ala	Leu	His	Arg	Gln	His	Arg	Gly	Met	Thr	Glu	Leu	Glu	Pro
		35				40						45			
Ser	Lys	Phe	Ser	Lys	Gln	Ala	Ala	Glu	Asn	Glu	Lys	Lys	Tyr	Tyr	Ile
	50					55					60				

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Glu	Lys	Leu	Phe	Glu	Arg	Tyr	Gly	Glu	Asn	Gly	Arg	Leu	Ser	Phe	Phe
65					70				75						80
Gly	Leu	Glu	Lys	Leu	Leu	Thr	Asn	Leu	Gly	Leu	Gly	Glu	Arg	Lys	Val
				85					90					95	
Val	Glu	Ile	Asn	His	Glu	Asp	Leu	Gly	His	Asp	His	Val	Ser	His	Leu
			100					105					110		
Gly	Ile	Leu	Ala	Val	Gln	Glu	Gly	Lys	His	Phe	His	Ser	His	Asn	His
		115					120					125			
Gln	His	Ser	His	Asn	His	Leu	Asn	Ser	Glu	Asn	Gln	Thr	Val	Thr	Ser
	130					135					140				
Val	Ser	Thr	Lys	Lys	Lys										
145					150										

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<213> Homo sapiens

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<222> -45...-1

<400> 197

Met	Asn	Trp	Ser	Ile	Phe	Glu	Gly	Leu	Leu	Ser	Gly	Val	Asn	Lys	Tyr
-45					-40					-35					-30
Ser	Thr	Ala	Phe	Gly	Arg	Ile	Trp	Leu	Ser	Leu	Val	Phe	Ile	Phe	Arg
				-25					-20					-15	
Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Glu	Arg	Val	Trp	Ser	Asp	Asp	His
			-10					-5					1		
Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys
5						10					15				
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
20					25					30					35
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				40					45					50	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
			55					60					65		
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		70				75						80			
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
	85					90						95			
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro
100					105					110					115
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
				120						125				130	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
			135					140					145		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
		150					155					160			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	165					170					175				
Met	Cys	Thr	Gly	His	His	Pro	His	Asp	Thr	Thr	Ser	Ser	Cys	Lys	Gln
180					185					190					195
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				200					205					210	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			215					220					225		

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Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro
	-35						-30					-25			
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
	-20					-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5					1				5					10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15					20						25		
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg
	30					35						40			
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45					50					55				
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60					65					70					75
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
			80					85						90	
His	Thr	Val	Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu
		95					100						105		
Gln	Ala	Val	Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys
	110						115						120		
Leu	Glu	Ala	Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val
	125					130					135				
Gln	Thr	Glu	Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser
140					145					150					155
Ile	Leu	Asn	Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu
			160						165					170	
Glu	Lys	Lys	Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val
			175				180						185		
Gln	Gln	Lys	Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg
	190						195					200			
Ser	Gln	Trp	Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met
	205					210					215				
Lys	Trp	Ser	Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys
220					225					230					235
Lys	Leu	Lys	Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln
			240						245					250	
Met	Phe	Arg	Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr
		255					260						265		
Leu	Asn	Ser	Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln
	270					275						280			
Arg	Gln	Val	Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr
	285					290					295				
Gly	Val	Leu	Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu
300					305					310					315
Val	Asp	Val	Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg
			320						325					330	
Thr	Tyr	Ser	Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg
		335					340						345		
Gln	Asn	Leu	Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile
	350						355					360			
Gly	Leu	Gln	Asn	Lys	Cys	Lys	Tyr	Gly	Ala	Lys	Lys	Lys			

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365	370	375															
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Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro																	
				-15					-10						-5		
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys																	
			1				5					10					
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg																	
			15			20					25						
Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His																	
			30		35				40							45	
Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp																	
				50				55							60		
Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr																	
			65				70							75			
Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln																	
			80			85						90					
Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp																	
			95		100						105						
Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu																	
			110		115				120								125
His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe																	
				130				135							140		
Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr																	
			145				150							155			
Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu																	
			160			165								170			
Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met																	
			175		180						185						
Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu																	
			190		195				200								205
Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met																	
				210				215								220	
Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe																	
			225				230								235		
Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn																	
			240			245						250					
Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys																	
			255		260						265						
Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met																	
			270		275				280								285
Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg																	
				290				295							300		
Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser																	
			305				310							315			
Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg																	
			320			325						330					
His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu																	
			335		340						345						
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln																	
			350		355				360								365

Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
370

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Met	Leu	Leu	Ser	Ile	Gly	Met	Leu	Met	Leu	Ser	Ala	Thr	Gln	Val	Tyr		
			-10					-5					1				
Thr	Val	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Pro	Leu	Pro	Val		
	5					10					15						
Glu	Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe		
20					25					30					35		
Asp	Asp	Leu	Pro	Ala	Arg	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu		
				40					45					50			
Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile		
			55					60					65				
Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu		
			70				75					80					
Ile	Arg	Arg	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln		
	85					90					95						
Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp		
100					105					110					115		
Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	Glu	Val	Leu	Lys	Lys	Ile	Asp		
				120					125					130			
Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp		
			135				140						145				
Glu	Phe	Thr	Tyr	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe		
		150					155					160					
Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Ile	Val	Gly		
	165					170				175							
Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Phe	Val	Gln		
180					185					190					195		
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys		
				200					205					210			
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys		
			215					220					225				
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu		
		230					235					240					
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr		
	245					250					255						
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser		
260					265					270					275		
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu		
				280					285					290			
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Ser	Val	Ser	Ala		
			295					300					305				
Gln	Ser	Phe	Gly	Ala	Leu	Ser	Glu	Ser	Arg	Ser	His	Gln	Asn	Met	Thr		
		310					315					320					
Glu	Ser	Ser	Asp	Tyr	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr	Asp	Ser	Ser		
	325					330				335							
Asp	Ala	Glu	Asn	Glu	Ile	Asn	Glu	His	Asp	Val	Val	Val	Gln	Leu	Gln		
340					345					350					355		
Pro	Asn	Gly	Glu	Arg	Asp	Tyr	Asn	Ile	Ala	Asn	Thr	Val					

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360

365

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Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe	
		-40					-35					-30				
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe	
	-25					-20					-15					
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp	
-10					-5				1					5		
Met	Cys	Leu	Lys	Ile	Ile	Arg	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg	
			10					15					20			
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu	
	25					30					35					
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val	
	40					45					50					
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr	
55					60					65					70	
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser	
			75					80						85		
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala	
			90					95					100			
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile	
	105						110					115				
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp	
	120					125					130					
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys	
135					140					145					150	
Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala	
			155						160					165		
Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu	
			170					175					180			
Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu	
	185					190						195				
Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val	
	200					205					210					
Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile	
215					220					225					230	
Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro	
			235						240					245		

Asn Lys Ala

<210> 202
 <211> 92
 <212> PRT
 <213> Homo sapiens
 <400> 202

Met	Pro	Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	
1				5				10						15		
Thr	Tyr	Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	
		20					25					30				
Asp	Arg	Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	

	35					40				45						
Cys	His	Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	
	50					55				60						
Gly	Ile	Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	
65					70					75					80	
Glu	Asn	Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser					
			85						90							

<210> 203
 <211> 127
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -63...-1
 <400> 203

Met	Ser	Ala	Ala	Gly	Ala	Arg	Gly	Leu	Arg	Ala	Thr	Tyr	His	Arg	Leu	
			-60					-55					-50			
Pro	Asp	Lys	Val	Glu	Leu	Met	Leu	Pro	Glu	Lys	Leu	Arg	Pro	Leu	Tyr	
		-45					-40					-35				
Asn	His	Pro	Ala	Gly	Pro	Arg	Thr	Val	Phe	Phe	Trp	Ala	Pro	Ile	Met	
	-30					-25					-20					
Lys	Trp	Gly	Leu	Val	Cys	Ala	Gly	Leu	Ala	Asp	Met	Ala	Arg	Pro	Ala	
-15					-10					-5					1	
Glu	Lys	Leu	Ser	Thr	Ala	Gln	Ser	Ala	Val	Leu	Met	Ala	Thr	Gly	Phe	
		5					10					15				
Ile	Trp	Ser	Arg	Tyr	Ser	Leu	Val	Ile	Ile	Pro	Lys	Asn	Trp	Ser	Leu	
	20					25						30				
Phe	Ala	Val	Asn	Phe	Phe	Val	Gly	Ala	Ala	Gly	Ala	Ser	Gln	Leu	Phe	
35					40					45						
Arg	Ile	Trp	Arg	Tyr	Asn	Gln	Glu	Leu	Lys	Ala	Lys	Ala	His	Lys		
50					55					60						

<210> 204
 <211> 84
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20...-1
 <400> 204

Met	Lys	Gly	Trp	Gly	Trp	Leu	Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly	
-20					-15					-10					-5	
Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg	
			1				5					10				
Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys	
	15					20					25					
Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln	
30					35					40						
Ser	Val	Val	Glu	Val	Thr	Val	Thr	Val	Pro	Pro	Asn	Lys	Val	Ala	His	
45					50					55					60	
Ser	Gly	Phe	Gly													

<210> 205
 <211> 182
 <212> PRT
 <213> Homo sapiens
 <220>

005T60"00999960
0063600"091500

<221> SIGNAL
<222> -20...-1
<400> 205

Met	Lys	Gly	Trp	Gly	Trp	Leu	Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly
-20					-15					-10					-5
Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg
			1				5					10			
Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys
	15					20					25				
Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln
30				35						40					
Ser	Val	Val	Glu	Val	Pro	Tyr	Ala	Arg	Ser	Glu	Ala	His	Leu	Thr	Glu
45				50						55					60
Leu	Leu	Glu	Glu	Ile	Cys	Asp	Arg	Met	Lys	Glu	Tyr	Gly	Glu	Gln	Ile
			65						70					75	
Asp	Pro	Ser	Thr	His	Arg	Lys	Asn	Tyr	Val	Arg	Val	Val	Gly	Arg	Asn
			80					85					90		
Gly	Glu	Ser	Ser	Glu	Leu	Asp	Leu	Gln	Gly	Ile	Arg	Ile	Asp	Ser	Asp
		95				100						105			
Ile	Ser	Gly	Thr	Leu	Lys	Phe	Ala	Cys	Gly	Ser	Ile	Val	Glu	Glu	Tyr
110					115						120				
Glu	Asp	Glu	Leu	Ile	Glu	Phe	Phe	Ser	Arg	Glu	Ala	Asp	Asn	Val	Lys
125				130						135					140
Asp	Lys	Leu	Cys	Ser	Lys	Arg	Thr	Asp	Leu	Cys	Asp	His	Ala	Leu	His
			145						150					155	
Ile	Ser	His	Asp	Glu	Leu										
			160												

<210> 206
<211> 71
<212> PRT
<213> Homo sapiens
<220>

<221> SIGNAL
<222> -25...-1
<400> 206

Met	Pro	Ala	Gly	Val	Pro	Met	Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala
-25					-20					-15					-10
Ser	Leu	Leu	Ala	Met	Cys	Ala	Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr
			-5					1				5			
Arg	Pro	Asp	Leu	Thr	Ile	Pro	Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu
	10					15					20				
Lys	Thr	Glu	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val
25					30						35				
Ser	Gln	Gln	Glu	Glu	Leu	Lys									
40					45										

<210> 207
<211> 73
<212> PRT
<213> Homo sapiens
<400> 207

Met	Arg	Ile	Arg	Met	Thr	Asp	Gly	Arg	Thr	Leu	Val	Gly	Cys	Phe	Leu
1				5					10					15	
Cys	Thr	Asp	Arg	Asp	Cys	Asn	Val	Ile	Leu	Gly	Ser	Ala	Gln	Glu	Phe
			20					25					30		
Leu	Lys	Pro	Ser	Asp	Ser	Phe	Ser	Ala	Gly	Glu	Pro	Arg	Val	Leu	Gly
	35						40					45			

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Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln Arg
 50 55 60
 Glu Ser Leu Thr Gly Pro Pro Tyr Leu
 65 70

<210> 208
 <211> 169
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -150..-1
 <220>
 <221> UNSURE
 <222> -67
 <223> Xaa = any one of the twenty amino acids
 <400> 208

Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys Asp
 -150 -145 -140 -135
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
 -130 -125 -120
 Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu Leu
 -115 -110 -105
 Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg Gly
 -100 -95 -90
 Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly Trp
 -85 -80 -75
 Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu
 -70 -65 -60 -55
 Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg
 -50 -45 -40
 Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr
 -35 -30 -25
 Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys
 -20 -15 -10
 Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser
 -5 1 5 10
 His Arg Ala Arg Gln Arg Lys Thr Ala
 15

<210> 209
 <211> 76
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22..-1
 <400> 209

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
 30 35 40
 Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
 45 50

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<210> 210
 <211> 95
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -54...-1
 <400> 210
 Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
 -50 -45 -40
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
 -35 -30 -25
 Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
 -20 -15 -10
 Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
 -5 1 5 10
 Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
 15 20 25
 Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
 30 35 40

<210> 211
 <211> 92
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22...-1
 <400> 211
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
 30 35 40
 Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
 45 50 55
 Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys
 60 65 70

<210> 212
 <211> 89
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -16...-1
 <400> 212
 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 -15 -10 -5
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1 5 10 15
 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 20 25 30
 Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile

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<400> 215

Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe	Leu	Tyr	Lys	Lys	Leu	Pro	Ser	Val
		-95					-90					-85			
Glu	Gly	Leu	His	Ala	Ile	Val	Val	Ser	Asp	Arg	Asp	Gly	Val	Pro	Val
	-80					-75					-70				
Ile	Lys	Val	Ala	Asn	Asp	Asn	Ala	Pro	Glu	His	Ala	Leu	Arg	Pro	Gly
-65					-60					-55					-50
Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly
				-45					-40					-35	
Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val
			-30					-25					-20		
Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser
		-15					-10					-5			
Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro
1					5					10					15
Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser				
				20					25						

<210> 216

<211> 93

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22...-1

<400> 216

Met	Lys	Pro	Val	Leu	Pro	Leu	Gln	Phe	Leu	Val	Val	Phe	Cys	Leu	Ala
		-20					-15					-10			
Leu	Gln	Leu	Val	Pro	Gly	Ser	Pro	Lys	Gln	Arg	Val	Leu	Lys	Tyr	Ile
	-5					1			5						10
Leu	Glu	Pro	Pro	Pro	Cys	Ile	Ser	Ala	Pro	Glu	Asn	Cys	Thr	His	Leu
				15					20					25	
Cys	Thr	Met	Gln	Glu	Asp	Cys	Glu	Lys	Gly	Phe	Gln	Cys	Cys	Ser	Ser
			30				35						40		
Phe	Cys	Gly	Ile	Val	Cys	Ser	Ser	Glu	Thr	Phe	Gln	Lys	Arg	Asn	Arg
		45					50					55			
Ile	Lys	His	Lys	Gly	Ser	Glu	Val	Ile	Met	Pro	Ala	Asn			
	60					65					70				

<210> 217

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 217

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
		-40					-35					-30			
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
	-25					-20				-15					
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Pro	Ile	Ile
-10					-5				1					5	
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
			10					15					20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys
		25				30						35			
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met

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40		45		50
Glu Gln Cys Gln Lys	Lys Pro Glu Asn Ser	Ala Glu Ser Asn Thr Glu		
55	60	65		70
Glu Thr Lys Arg Thr	Asp Leu Thr Gln Asp	Asp Phe His Leu Lys Ile		
	75	80		85
Leu Lys Asp Ile Leu	Cys Glu Phe Leu Ser	Asn Ile Phe Gln Ala Leu		
	90	95		100
Thr Lys Glu Thr Val	Ala Gln Gly Val Lys	Glu Gly Gln Leu Ser Lys		
	105	110		115
Gln Lys Cys Ser Ser	Ala Phe Gln Asn Leu	Leu Pro Phe Tyr Ser Pro		
	120	125		130
Val Val Glu Asp Phe	Ile Lys Ile Leu Arg	Glu Val Asp Lys Ala Leu		
135	140	145		150
Ala Asp Asp Leu Glu	Lys Asn Phe Pro Ser	Leu Lys Val Gln Thr		
	155	160		165

<210> 218

<211> 59

<212> PRT

<213> Homo sapiens

<400> 218

Met Pro His Ser Lys	Pro Leu Asp Trp	Gly Leu Ser Ser	Val Ala Glu
1	5	10	15
Cys Pro Ala Glu Leu	Phe Pro Ser Thr	Gly Gly Leu Ala	Gly Lys Gly
	20	25	30
Pro Gly Leu Asp Ile	Leu Arg Cys Val	Leu Ser Pro Trp	Ala Ser His
	35	40	45
Phe Pro Ser Leu Ser	Leu Gly Val Phe	Asn Leu	
50	55		

<210> 219

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 219

Met Asn Arg Val Pro	Ala Asp Ser Pro	Asn Met Cys Leu	Ile Cys Leu
	-25	-20	-15
Leu Ser Tyr Ile Ala	Leu Gly Ala Ile	His Ala Lys Ile	Cys Arg Arg
	-10	-5	1
Ala Phe Gln Glu Glu	Gly Arg Ala Asn	Ala Lys Thr Gly	Val Arg Ala
	10	15	20
Trp Cys Ile Gln Pro	Trp Ala Lys		
	25		

<210> 220

<211> 162

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -94...-1

<400> 220

Met Leu Gln Thr Ser	Asn Tyr Ser Leu	Val Leu Ser Leu	Gln Phe Leu
	-90	-85	-80
Leu Leu Ser Tyr Asp	Leu Phe Val Asn	Ser Phe Ser Glu	Leu Leu Gln

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			-75					-70					-65			
Lys	Thr	Pro	Val	Ile	Gln	Leu	Val	Leu	Phe	Ile	Ile	Gln	Asp	Ile	Ala	
		-60					-55					-50				
Val	Leu	Phe	Asn	Ile	Ile	Ile	Ile	Phe	Leu	Met	Phe	Phe	Asn	Thr	Phe	
	-45					-40					-35					
Val	Phe	Gln	Ala	Gly	Leu	Val	Asn	Leu	Leu	Phe	His	Lys	Phe	Lys	Gly	
-30				-25				-20							-15	
Thr	Ile	Ile	Leu	Thr	Ala	Val	Tyr	Phe	Ala	Leu	Ser	Ile	Ser	Leu	His	
			-10					-5						1		
Val	Trp	Val	Met	Asn	Leu	Arg	Trp	Lys	Asn	Ser	Asn	Ser	Phe	Ile	Trp	
	5					10					15					
Thr	Asp	Gly	Leu	Gln	Met	Leu	Phe	Val	Phe	Gln	Arg	Leu	Ala	Ala	Val	
20					25					30						
Leu	Tyr	Cys	Tyr	Phe	Tyr	Lys	Arg	Thr	Ala	Val	Arg	Leu	Gly	Asp	Pro	
35				40					45						50	
His	Phe	Tyr	Gln	Asp	Ser	Leu	Trp	Leu	Arg	Lys	Glu	Phe	Met	Gln	Val	
			55					60						65		

Arg Arg

<210> 221

<211> 154

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68...-1

<400> 221

Met	Ala	Ser	Ala	Ser	Ala	Arg	Gly	Asn	Gln	Asp	Lys	Asp	Ala	His	Phe	
		-65					-60					-55				
Pro	Pro	Pro	Ser	Lys	Gln	Ser	Leu	Leu	Phe	Cys	Pro	Lys	Ser	Lys	Leu	
	-50				-45					-40						
His	Ile	His	Arg	Ala	Glu	Ile	Ser	Lys	Ile	Met	Arg	Glu	Cys	Gln	Glu	
-35					-30					-25						
Glu	Ser	Phe	Trp	Lys	Arg	Ala	Leu	Pro	Phe	Ser	Leu	Val	Ser	Met	Leu	
-20				-15				-10							-5	
Val	Thr	Gln	Gly	Leu	Val	Tyr	Gln	Gly	Tyr	Leu	Ala	Ala	Asn	Ser	Arg	
		1				5					10					
Phe	Gly	Ser	Leu	Pro	Lys	Val	Ala	Leu	Ala	Gly	Leu	Leu	Gly	Phe	Gly	
	15				20					25						
Leu	Gly	Lys	Val	Ser	Tyr	Ile	Gly	Val	Cys	Gln	Ser	Lys	Phe	His	Phe	
30					35				40							
Phe	Glu	Asp	Gln	Leu	Arg	Gly	Ala	Gly	Phe	Gly	Pro	Gln	His	Asn	Arg	
45				50				55							60	
His	Cys	Leu	Leu	Thr	Cys	Glu	Glu	Cys	Lys	Ile	Lys	His	Gly	Leu	Ser	
			65					70						75		
Glu	Lys	Gly	Asp	Ser	Gln	Pro	Ser	Ala	Ser							
		80						85								

<210> 222

<211> 99

<212> PRT

<213> Homo sapiens

<400> 222

Met	Lys	Val	Glu	Glu	Glu	His	Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly	
1		5						10					15			
Gly	Leu	Thr	Ala	Thr	Leu	Val	Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu	
		20					25					30				
Cys	Thr	Glu	Arg	Gly	Ala	Pro	Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr	

35 40 45
 Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr Ala His
 50 55 60
 Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Gly Leu Thr
 65 70 75 80
 Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr Lys His
 85 90 95
 Leu Gly Asn

<210> 223
 <211> 43
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -24...-1
 <400> 223

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -20 -15 -10
 Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
 -5 1 5
 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
 10 15

<210> 224
 <211> 69
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -21...-1
 <400> 224

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Gln Lys
 45

<210> 225
 <211> 78
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -18...-1
 <400> 225

Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
 -15 -10 -5
 Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
 1 5 10
 Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
 15 20 25 30
 Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val

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				35					40				45
Val	Thr	Val	Gly	Gly	Gly	Arg	Val	Gly	Ser	Thr	Phe	Val	Ala
			50					55					60

<210> 226
 <211> 80
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -47...-1
 <400> 226

Met	Arg	Leu	Pro	Pro	Ala	Leu	Pro	Ser	Gly	Tyr	Thr	Asp	Ser	Thr	Ala
		-45					-40					-35			
Leu	Glu	Gly	Leu	Val	Tyr	Tyr	Leu	Asn	Gln	Lys	Leu	Leu	Phe	Ser	Ser
	-30					-25					-20				
Pro	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Ala	Arg	Pro	Cys	Val	Phe	Cys	Phe
-15					-10				-5						1
Lys	Ala	Ser	Lys	Met	Gly	Pro	Gln	Phe	Glu	Asn	Tyr	Pro	Thr	Phe	Pro
		5					10					15			
Thr	Tyr	Ser	Pro	Leu	Pro	Ile	Ile	Pro	Phe	Gln	Leu	His	Gly	Arg	Phe
		20					25					30			

<210> 227
 <211> 241
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -103...-1
 <400> 227

Met	Trp	Leu	Asp	Pro	Val	Phe	Pro	Leu	Phe	Pro	Val	Gly	Asp	His	Tyr
		-100					-95					-90			
Leu	Pro	His	Leu	His	Met	Asp	Val	Leu	Glu	Gly	Leu	Ile	Leu	Val	Leu
	-85					-80					-75				
Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val	Thr	Cys
	-70				-65				-60						
Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr	Thr	Gln
-55				-50					-45						-40
Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser	Ala	Val
			-35				-30						-25		
Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala	Gln	Thr
	-20						-15					-10			
Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile	Leu	Ala
	-5				1					5					
Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp	Asp	Ala
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			30					35					40		
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		45					50					55			
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	60					65						70			
Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu	Ser	Pro
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